



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 131428

TO: Rosanne Kosson
Location: rem/3b84/3e71
Art Unit: 1651
September 8, 2004

Case Serial Number: 10/619149

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

131 428

my

From: Kosson, Rosanne
Sent: Tuesday, August 31, 2004 5:59 PM
To: STIC-Biotech/ChemLib
Cc: Prats, Frank
Subject: request for sequence search

Could you search a sequence for me- application no. 10/619,149, SEQ ID NO: 1, which is a protein sequence (human PEDF)? Please let me know if you need any additional info for the conducting the searches. Thanks!!!

Rosanne Kosson
Patent Examiner, AU 1651
REM 3B84
571-272-2923
rosanne.kosson@uspto.gov

3E71

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Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 1, 2004, 10:58:23 ; Search time 125 Seconds
(without alignments)
944.839 Million cell updates/sec

Title: US-10-619-149-1
Perfect score: 2131
Sequence: 1 MQALVLLICIGALLGHSSCO.....RDTDTGALLFIGKILDPGRP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseqp_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2125	99.7	418	2 AAR90287	Aar90287 Pigment e
2	2125	99.7	418	4 AAE10306	Aae10306 Human pig
3	2125	99.7	418	5 ABB81091	Abb81091 Human pig
4	2125	99.7	418	6 AAE38136	Aae38136 Human ret
5	2125	99.7	418	7 ABUI10031	Abui10031 Human pig
6	2106	98.8	418	2 AAR44800	Aar44800 Sequence
7	2106	98.8	418	6 ABR58379	Abr58379 Human NOV
8	2097	98.4	418	6 ABR72122	Abg72122 Human pig
9	2097	98.4	418	7 ADB99089	Adb99089 Human ret
10	1904	89.3	379	2 AAR90288	Aar90288 Modified
11	1870	87.8	379	6 ABR72123	Abg72123 Truncated
12	1870	87.8	379	7 ADB99090	Adb99090 Human ret
13	1789	84.0	418	5 ABB57391	Abb57391 Rat mucoc
14	1784	83.7	362	2 AAR97364	Aar97364 Amino aci
15	1784	83.7	362	4 AAU08652	Aau08652 Human ant
16	1784	83.7	362	5 ABB08433	Abb08433 SLED poly
17	1784	83.7	362	5 ABB04587	Abb04587 Human ant
18	1651	77.5	362	4 AAE10305	Aae10305 Human pig
19	499	23.4	125	4 AAB87625	Aab87625 Bovine ma
20	472	22.1	111	3 AAG031717	Agag031717 Human sec
21	464.5	21.8	491	3 AAY59193	Aay59193 Mouse alp
22	458.5	21.5	124	4 AAO07150	Aao07150 Human pol
23	457.5	21.5	491	3 AAY59192	Aay59192 Bovine alp
24	457	21.4	490	2 AAR04252	Aar04252 Amino aci
25	456.5	21.4	488	3 AAY59191	Aay59191 Human alp

26	456.5	21.4	491	2 AAR13860	Aar13860 Human alp
27	456	21.4	492	1 AAP90486	Aap90486 Human alp
28	455	21.4	452	1 AAP90534	Aap90534 Peptide s
29	455	21.4	464	2 AAR05411	Aar05411 Pro-type
30	450.5	21.1	744	1 AAP81006	Aap81006 Alpha-2-p
31	444	20.8	413	5 ABR91415	Abg91415 Primate L
32	432.5	20.3	503	5 AAU99881	Aau99881 SLAP1 fus
33	432	20.3	418	1 AAP50021	Aap50021 Sequence
34	430	20.2	417	3 AAB36101	Aab36101 Human alp
35	430	20.2	417	3 AAB26705	Aab26705 Human alp
36	430	20.2	417	7 ADE34542	Ade34542 Human alp
37	430	20.2	418	2 AAR22931	Aar22931 Alpha-1-a
38	429.5	20.2	413	2 AAW23138	Aaw23138 Protease
39	429	20.1	418	6 ABR48498	Abr48498 Human Alp
40	428	20.1	418	7 ADE60631	Ade60631 Human Pro
41	428	20.1	418	7 ADD45920	Add45920 Human Pro
42	427	20.0	394	2 AAR67362	Aar67362 Alpha-1-a
43	427	20.0	418	1 AAP40133	Aap40133 Sequence
44	427	20.0	418	1 AAP94664	Aap94664 Predomina
45	427	20.0	418	2 AAY26925	Aay26925 Human alp

ALIGNMENTS

RESULT 1
AAR90287
ID AAR90287 standard; protein; 418 AA.
XX
AC AAR90287;
XX
DT 16-JAN-1997 (first entry)
XX
DE Pigment epithelium-derived factor.
XX
KW Pigment epithelium-derived factor; PEDF; neuronal cells; neurons;
glial cells; gliastatic; gliosis; central nervous system; CNS;
KW Neurodegenerative disease; injury; neurotrophic; brain cells;
KW Parkinson's disease; photoreceptor cells; retina; inhibition;
KW Proliferation; immunoassay; antibody; ageing; degenerative disease.
XX
OS Homo sapiens.
XX
PN WO9533480-A1.
XX
PD 14-DEC-1995.
XX
PF 06-JUN-1995; 95WO-US007201.
XX
PR 07-JUN-1994; 94US-00257963.
PR 30-DEC-1994; 94US-00367841.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chader GJ, Becerra SP, Schwartz JP, Taniwaki T;
XX
DR WPI; 1996-039966/04.
DR N-PSDB; AAT11658.
XX
PT Use of pigment epithelium derived factor - for enhancing neuronal cell
survival and inhibiting glial cell proliferation, useful, e.g. in CNS
cell culture or to treat neuro-degenerative diseases.
XX
PS Disclosure; Page 64-65; 151pp; English.
XX
CC Pigment epithelium-derived factor (PEDF) has both neurotrophic and
gliastatic activity, making it useful in cases where neurons die quickly
and glia tend to proliferate (gliosis), e.g. in CNS cell culture, in
CC neurodegenerative diseases and in CNS injury. The neurotrophic effect
of PEDF is especially useful for enhancing survival of neuronal cell
cultures intended for use in transplantation. These include cultures of
human foetal brain cells and neural retina and photoreceptor cells. The
gliastatic activity of PEDF can be applied to inhibiting glial cell

CC proliferation in certain tumours. Antibodies directed against PEDF can be
 CC used for inhibiting PEDF activity or in an immunoassay for determining
 CC levels of PEDF in fluid, cellular or tissue samples e.g for determining
 CC ageing and/or other degenerative diseases
 XX
 SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 2; Length 418;
 Best Local Similarity 99.5%; Pred. No. 3.3e-189;
 Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLAAAVSN 60
 Db 1 MQALVLLLCIGALLGHSSCONPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLAAAVSN 60

Qy 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDH 120
 Db 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGADERTESIHRALYYDLISSPDH 120

Qy 121 TYKELDTVTAPQKNLSASRIVFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180
 Db 121 TYKELDTVTAPQKNLSASRIVFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180

Qy 181 NNWQAMKGLARSTKEIPDEISILLGVAFKQGVTKFDSRKTSLEDFYLDERTVR 240
 Db 181 NNWQAMKGLARSTKEIPDEISILLGVAFKQGVTKFDSRKTSLEDFYLDERTVR 240

Qy 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMISIFFLPKVTQNTLIEESITSEFIH 300
 Db 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMISIFFLPKVTQNTLIEESITSEFIH 300

Qy 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360

Qy 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDRTDGTGALLFGKILDPRGP 418
 Db 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDRTDGTGALLFGKILDPRGP 418

RESULT 2
 AA10306
 ID AA10306 standard; protein; 418 AA.
 XX
 AC AA10306;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human pigment epithelium derived growth factor (PEDF).
 XX
 KW Human; pigment epithelium derived growth factor; PEDF; angiogenesis;
 KW tumour; benign neoplasia; ischaemic retinopathy; macular degeneration;
 KW scleroderma; infection; cat scratch disease; muscle active general;
 KW bacterial ulceration; diabetic retinopathy; neuroblastoma; haemangioma;
 KW muscle disease; myocardial angiogenesis; arthritis; haemophilic joint;
 KW Osler-Webber Syndrome; plaque neovascularisation; telangiectasia;
 KW angiofibroma; wound granularisation; cytostatic; therapy; psoriasis;
 KW antiinflammatory; antipsoriatic; antiviral; antidiabetic;
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 318
 FT /note= "Encoded by AGG"
 XX
 PN W0200162725-A2.
 XX
 PD 30-AUG-2001.
 XX
 XX 22-FEB-2001; 2001WO-US005915.
 XX
 XX 23-FEB-2000; 2000US-00511683.
 XX
 PR 23-JUN-2000; 2000US-00603478.
 PR

XX (NOUN) UNIV NORTHWESTERN.
 PA Bouck NP, Dawson DW, Gillis PR, Crawford SE, Stellmach VM;
 XX Volpert O;
 PI
 XX WPI; 2001-582032/65.
 DR N-PSDB; AAD17438.
 XX
 XX Inhibiting angiogenesis within a tissue in a mammal, comprises providing
 PT exogenous pigment epithelium derived growth factor (PEDF) systemically to
 PT the mammal, useful for treating ischemic retinopathy, macular
 PT degeneration and psoriasis.
 XX
 PS Claim 20; Page 96-98; 100pp; English.

XX The invention relates to a method of inhibiting angiogenesis within a
 CC tissue by providing exogenous pigment epithelium derived growth factor
 CC (PEDF) to cells associated with the tissue. The presence of exogenous
 CC PEDF inhibits angiogenesis within the tissue, in part by interfering with
 CC the ability of vascular endothelia to expand within the tissue. The
 CC invention also provides a method for determining the severity of a tumour
 CC by assaying for the presence of PEDF within the tumour. PEDF inhibits
 CC angiogenesis within the tissue and is useful for treating a benign
 CC neoplasia of a nasal polyp or the prostate gland, ischaemic retinopathy
 CC and macular degeneration. PEDF is useful for treating diseases and
 CC disorders such as psoriasis, scleroderma, tumours of the skin,
 CC neovascularisation as a consequence of infection (e.g., cat scratch
 CC disease, bacterial ulceration, etc.), diabetic retinopathy, a tumour
 CC (e.g., a benign or cancerous growth), and childhood tumours (including,
 CC but not limited to, neuroblastoma). PEDF can also be used for treating
 CC disorders of blood vessels (e.g., haemangiomas), muscle diseases (e.g.,
 CC myocardial angiogenesis or angiogenesis within smooth muscles), joints
 CC (e.g., arthritis, haemophilic joints, etc.), and other disorders
 CC associated with angiogenesis (e.g., Osler-Webber Syndrome, plaque
 CC neovascularisation, telangiectasia, angiofibroma, wound granularisation,
 CC etc.). PEDF can also retard the growth of existing tumours. The present
 CC sequence is human PEDF protein. Note: this sequence SEQ.ID.NO.1 is stated
 CC to be similar to the sequence shown in Fig 6A (AA10305). However this
 CC sequence differs at several locations from the sequence shown in Fig 6A
 XX
 SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 4; Length 418;
 Best Local Similarity 99.5%; Pred. No. 3.3e-189;
 Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLAAAVSN 60
 Db 1 MQALVLLLCIGALLGHSSCONPASPPEEGSPDPDSTGALVEEDPFFKVPVVKLAAAVSN 60

Qy 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGAEQRTESIHRALYYDLISSPDH 120
 Db 61 FGVDLYVRSSMSTTNVLLSPVATALSALSGADERTESIHRALYYDLISSPDH 120

Qy 121 TYKELDTVTAPQKNLSASRIVFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180
 Db 121 TYKELDTVTAPQKNLSASRIVFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRLDLQEI 180

Qy 181 NNWQAMKGLARSTKEIPDEISILLGVAFKQGVTKFDSRKTSLEDFYLDERTVR 240
 Db 181 NNWQAMKGLARSTKEIPDEISILLGVAFKQGVTKFDSRKTSLEDFYLDERTVR 240

Qy 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMISIFFLPKVTQNTLIEESITSEFIH 300
 Db 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMISIFFLPKVTQNTLIEESITSEFIH 300

Qy 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLFDSPFSKITGPKIKLTQVEHRA 360

Qy 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDRTDGTGALLFGKILDPRGP 418
 Db 361 GFENWEDGAGTTSPGLOPAHLTPFLDYHLNQPFIFVLRDRTDGTGALLFGKILDPRGP 418

Db 361 GFEWNEGAGTTPSGQLPAHLTFPLDYHLNQPFIFVLRTDTGALLFIGKILDRGP 418

RESULT 3

ABB81091

ID ABB81091 standard; protein; 418 AA.

XX AC ABB81091;

XX DT 05-NOV-2002 (first entry)

XX DE Human pigment epithelium-derived factor (PEDF) sequence.

XX KW PEDF; choroidal neovascularization; photoactive; ocular; antidiabetic;

XX KW ophthalmological; photodynamic therapy; retina; angiogenic; human;

XX KW pigment epithelium-derived factor.

XX OS Homo sapiens.

XX FN WO200258730-A2.

XX PD 01-AUG-2002.

XX PF 26-OCT-2001; 2001WO-US051062.

XX PR 01-NOV-2000; 2000US-0244850P.

XX PA (ALLR) ALLERGAN SALES INC.

XX PI Wheeler LA, De Vries GW;

XX DR WPI; 2002-619144/66.

XX PT Treatment useful for choroidal neovascularization involves combining

XX PT photodynamic therapy with the administration of an antiangiogenic

XX PT compound.

XX PS Disclosure; Page 4; 33pp; English.

XX CC The invention relates to the treatment of choroidal neovascularization

XX CC that involves administering a photoactive compound to localize the

XX CC affected target ocular tissue, irradiating the tissue with light emitted

XX CC from a laser at a wavelength for absorption by the photoactive compound

XX CC and then administering an antiangiogenic compound to inhibit recurrence

XX CC of neovascularization. The method is useful for the treatment of

XX CC choroidal neovascularization and to protect ocular neural tissue from

XX CC damage caused by photodynamic therapy; and also for the treatment of

XX CC diabetic retinopathy. The method is more selective closure of blood

XX CC vessels, in order to preserve the overlying neurosensory retina. This

XX CC method is safer than photocoagulation. The present sequence represents

XX CC the human pigment epithelium-derived factor (PEDF), used as the

XX CC antiangiogenic compound in the method of the invention.

XX SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 5; Length 418;

Best Local Similarity 99.5%; Pred. No. 3.3e-189;

Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Db 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALCAQRTESIHRALYYDLISSPDING 120

Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALCAQRTESIHRALYYDLISSPDING 120

Qy 121 TYKELLDVTVAQPNKLSASIVFEKKLRIRKSSFVAPLEKSYGTRPRVLGNPRLDLOEI 180

Db 121 TYKELLDVTVAQPNKLSASIVFEKKLRIRKSSFVAPLEKSYGTRPRVLGNPRLDLOEI 180

Qy 181 NNWQAOQMKGLARSTKEIPDEISILLGVAFHKQGWTKFDSRKTSLIEDFYLDERTVR 240

Db 181 NNWQAOQMKGLARSTKEIPDEISILLGVAFHKQGWTKFDSRKTSLIEDFYLDERTVR 240

Qy 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMSIIFFLPLKVTQNTLIEESLTSEFIHD 300

Db 241 VPMMSDPKAVLRGLDSDLCKIAQLPLTGSMSIIFFLPLKVTQNTLIEESLTSEFIHD 300

Qy 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQENKLSLSDSPDPSFKITGKPIKLTQVEHRA 360

Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQENKLSLSDSPDPSFKITGKPIKLTQVEHRA 360

Qy 361 GFEWNEGAGTTPSGQLPAHLTFPLDYHLNQPFIFVLRTDTGALLFIGKILDRGP 418

Db 361 GFEWNEGAGTTPSGQLPAHLTFPLDYHLNQPFIFVLRTDTGALLFIGKILDRGP 418

RESULT 4

AAE38136

ID AAE38136 standard; protein; 418 AA.

XX AC AAE38136;

XX DT 20-NOV-2003 (first entry)

XX DE Human retinal pigment epithelium derived factor (PEDF).

XX KW Human; pigment epithelium derived factor; PEDF; diabetic retinopathy;

XX KW anti-angiogenic; neurotrophic; gliastatic; therapy; cell proliferation;

XX KW age-related macular degeneration; neuronal disease; retinal detachment;

XX KW tumour.

XX OS Homo sapiens.

XX FN WO2003059248-A2.

XX PD 24-JUL-2003.

XX PF 02-JAN-2003; 2003WO-IL0000007.

XX PR 03-JAN-2002; 2002IL-00147444.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Shaltiel S, Schwartz I;

XX DR WPI; 2003-598472/56.

XX PT New isolated pigment epithelium derived factor (PEDF) or its fragment or

XX PT derivative isolated from plasma or its salt, useful for preparing a

XX PT composition for treating neuronal or angiogenesis-related disease, e.g.,

XX PT choroidal tumors.

XX PS Disclosure; Page 57-58; 60pp; English.

XX CC The invention relates to pigment epithelium derived factor (PEDF)

XX CC comprising inhibitory activity of endothelial cell proliferation, anti-

XX CC angiogenic activity, neurotrophic activity, neurotrophic activity or

XX CC gliastatic activity. The PEDF is useful for preparing a composition for

XX CC treating neuronal disease or angiogenesis-related disease, e.g., age-

XX CC related macular degeneration, diabetic retinopathy, retinal detachment,

XX CC retinal tumours and choroidal tumours. The present sequence is human

XX CC retinal PEDF protein

XX SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 6; Length 418;

Best Local Similarity 99.5%; Pred. No. 3.3e-189;

Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Db 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEDPFFKVPVKNKLAASN 60

Qy 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALCAQRTESIHRALYYDLISSPDING 120

Db 61 FGDLVRRSSMSTTNVLLSPLSVATALSALGADERTESIHRALYYDLISSPDH 120
 QY 121 TYKELDTVTAPQKNLKSASRIVEFKLRKSSVAPLEKSYGTRPRVLTGNRLDLOEI 180
 Db 121 TYKELDTVTAPQKNLKSASRIVEFKLRKSSVAPLEKSYGTRPRVLTGNRLDLOEI 180
 QY 181 NNWVQAQMGKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
 Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
 QY 241 VPMMSDKAVLRYGLDSLSCKIAQLPLTGSMSIIFPLPLKVTQNTLIEESLTSFIHD 300
 Db 241 VPMMSDKAVLRYGLDSLSCKIAQLPLTGSMSIIFPLPLKVTQNTLIEESLTSFIHD 300
 QY 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 QY 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418
 Db 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418

RESULT 5

ABU10031
 ID ABU10031 standard; protein; 418 AA.
 XX
 AC ABU10031;
 XX
 DT 06-AUG-2003 (first entry)
 XX
 DE Human pigment epithelium-derived factor PEDF.

Human; pigment epithelium-derived growth factor; PEDF; cytostatic; antiarteriosclerotic; antidiabetic; ophthalmological; antiarthritic; gene therapy; Wilms' tumour; prostate cancer; cancer; neovascularisation; haemangioma; atherosclerosis; diabetic retinopathy; arthritis; pre-cancerous lesion; nasal polyp.

OS Homo sapiens.

XX US2003064917-A1.

XX 03-APR-2003.

XX 26-JUN-2002; 2002US-00180959.

XX 23-JUL-1998; 98US-00122079.

XX 23-JUL-1998; 98WO-US015228.

XX 23-FEB-2000; 2000US-00511683.

XX 23-JUN-2000; 2000US-00603478.

XX (CRAW/) CRAWFORD S E.

XX (DOLL/) DOLL J A.

XX (STELL/) STELLMACH V.

XX Crawford SE, Doll JA, Stellmach V;

XX WPI; 2003-467440/44.

XX N-PSDB; ACA61620.

XX Treating Wilms' tumor or prostate cancer in a mammal comprises providing an exogenous PEDF to the mammal to treat the tumor or cancer.

XX Example 6; Fig 6A; 66pp; English.

XX The invention describes a method of treating Wilms' tumour or prostate cancer in a mammal comprising providing an exogenous PEDF to the mammal to treat the tumour or cancer.

XX determining the severity of Wilms' tumour or prostate cancer in a mammal. The method may also be used in preventing or treating other disorders associated with neovascularisation, such as haemangioma, atherosclerosis,

CC diabetic retinopathy, arthritis, and other pre-cancerous lesions like nasal polyps. This is the amino acid sequence of human pigment epithelium-driven factor (PEDF)
 CC
 XX
 SQ Sequence 418 AA;

Query Match 99.7%; Score 2125; DB 7; Length 418;
 Best Local Similarity 99.5%; Pred. No. 3.3e-189;
 Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALVLLLCIGALLGHSSCONPSPPEEGSPDPDSTGALVEEEDPPFKVPVKNLAAAVSN 60
 Db 1 MQALVLLLCIGALLGHSSCONPSPPEEGSPDPDSTGALVEEEDPPFKVPVKNLAAAVSN 60
 QY 61 FGDLVRRSSMSTTNVLLSPLSVATALSALGADERTESIHRALYYDLISSPDH 120
 Db 61 FGDLVRRSSMSTTNVLLSPLSVATALSALGADERTESIHRALYYDLISSPDH 120
 QY 121 TYKELDTVTAPQKNLKSASRIVEFKLRKSSVAPLEKSYGTRPRVLTGNRLDLOEI 180
 Db 121 TYKELDTVTAPQKNLKSASRIVEFKLRKSSVAPLEKSYGTRPRVLTGNRLDLOEI 180
 QY 181 NNWVQAQMGKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
 Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVHAHFGQWVTKFDSKTSLEDFYLDERTVR 240
 QY 241 VPMMSDKAVLRYGLDSLSCKIAQLPLTGSMSIIFPLPLKVTQNTLIEESLTSFIHD 300
 Db 241 VPMMSDKAVLRYGLDSLSCKIAQLPLTGSMSIIFPLPLKVTQNTLIEESLTSFIHD 300
 QY 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTQVAVLTVPKLSYEGEVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 QY 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418
 Db 361 GFENWEDGAGTTPSPGLQPAHLTPPLDYHLNQPFIFVLRDTDTGALLFIGKILDPGRP 418

RESULT 6

AAR44800
 ID AAR44800 standard; protein; 418 AA.
 XX
 AC AAR44800;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-JUN-1994 (first entry)

DE Sequence of retinal pigmented epithelium-derived neurotrophic factor (PEDNF).
 DE

XX Serine protease inhibitor gene family; neurotrophic activity; tumour therapy.
 KW
 XX Homo sapiens.

XX WO9324529-A1.
 PN
 XX 09-DEC-1993.

XX 04-JUN-1993; 93WO-US005358.
 PF
 XX 04-JUN-1992; 92US-00894215.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
 PA
 XX Johnson IV, Tombran-Tink J;

XX WPI; 1993-405734/50.
 DR
 XX N-PSDB; AAQ53160.

XX Purified retinal pigmented epithelium derived neurotrophic factor - is used for treating tumours, ocular disease or nerve damage or as serine
 PT

PT protease inhibitors for treating e.g. ischaemia, etc.
 XX Claim 1; Page 44-46; 55pp; English.
 PS PEDNF was isolated from cultured retinal pigment epithelium (RPE) cells.
 XX Oligos were constructed from the sequence derived from PEDNF and used as
 CC primers in PCR amplification of a human fetal eye Charon BS cDNA library
 CC to obtain DNA encoding PEDNF. The oligo primers were constructed against
 CC the following peptides: PEDNF 13 - residues 236- 244 (AAQ53161); and
 CC PEDNF 2 - residues 107-135 (AAQ53162). PEDNF is a unique member of the
 CC serine protease inhibitor (SERPIN) gene family. (Updated on 25-MAR-2003
 CC to correct FN field.)
 XX Sequence 418 AA;
 SQ

Query Match 98.8%; Score 2106; DB 2; Length 418;
 Best Local Similarity 99.0%; Pred. No. 2e-187;
 Matches 414; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGGPDSTGALVEEDPPFKVPVKNKLAASN 60
 Db 1 MQALVLLLCIGALLGHSSWQNPASPPEGGPDSTGALVEEDPPFKVAVNKLAAVSN 60
 Qy 61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGAQRTESIHRALYYDLISSPDH 120
 Db 61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGADERTESIHRALYYDLISSPDH 120
 Qy 121 TYKELDTVTAPQKNLKSASRIVFEEKLRKSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
 Db 121 TYKELDTVTAPQKNLKSASRIVFEEKLRKSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
 Qy 181 NNWVQAMQKGLARSTKEIPDEISILLGLVAHFGQWTKFDSRKTSLEDFYLDERTVR 240
 Db 181 NNWVQAMQKGLARSTKEIPDEISILLGLVAHFGQWTKFDSRKTSLEDFYLDERTVR 240

RESULT 7
 ABR58379 standard; protein; 418 AA.
 XX ABR58379;
 XX 07-JUL-2003 (first entry)
 XX Human NOV7a.
 XX Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective; dyslipidaemia;
 KW antiparkinsonian; antilipaeic; gene therapy; metabolic disorder;
 KW diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;
 KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
 KW haematopoietic disorder.
 XX Homo sapiens.
 XX WO2003029423-A2.
 XX 10-APR-2003.
 XX 02-OCT-2002; 2002WO-US031358.

PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327342P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328449P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 22-OCT-2001; 2001US-0341059P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 12-APR-2002; 2002US-0371972P.
 PR 12-APR-2002; 2002US-0371980P.
 PR 17-APR-2002; 2002US-0373261P.
 PR 19-APR-2002; 2002US-0373805P.
 PR 23-APR-2002; 2002US-0374738P.
 PR 16-MAY-2002; 2002US-0381101P.
 PR 17-MAY-2002; 2002US-0381635P.
 PR 29-MAY-2002; 2002US-0383830P.
 PR 01-OCT-2002; 2002US-00262839.
 XX (CURA-) CURAGEN CORP.
 XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E;
 PI Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W;
 PI Kekua R, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK;
 PI Rothenberg ME, Shinkens RA, Smithson G, Spytek RA, Taupier RJ;
 PI Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
 XX WPI; 2003-381625/36.
 DR N-PSDB; ACC72091.
 XX NOVX polypeptides and nucleic acids useful for diagnosing, preventing or
 PT treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or
 PT dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX Claim 1; Page 129; 487pp; English.
 XX The present invention relates to novel human NOV proteins and their
 CC coding sequences (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV
 CC proteins are useful in manufacturing a medicament for treating a syndrome
 CC associated with a human disease. The NOV proteins and coding sequences
 CC may be used to diagnose, treat or prevent metabolic disorders such as
 CC diabetes or obesity, infections, cachexia, cancer, neurodegenerative
 CC disorders such as Alzheimer's disease or Parkinson's disease, immune
 CC disorders, haematopoietic disorders and various dyslipidaemias
 XX Sequence 418 AA;
 SQ

Query Match 98.8%; Score 2106; DB 6; Length 418;
 Best Local Similarity 99.0%; Pred. No. 2e-187;
 Matches 414; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGGPDSTGALVEEDPPFKVPVKNKLAASN 60
 Db 1 MQALVLLLCIGALLGHSSWQNPASPPEGGPDSTGALVEEDPPFKVAVNKLAAVSN 60
 Qy 61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGAQRTESIHRALYYDLISSPDH 120
 Db 61 FGVDLYRVSSMPTTNVLLSPLSVATALSALSGADERTESIHRALYYDLISSPDH 120
 Qy 121 TYKELDTVTAPQKNLKSASRIVFEEKLRKSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
 Db 121 TYKELDTVTAPQKNLKSASRIVFEEKLRKSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
 Qy 181 NNWVQAMQKGLARSTKEIPDEISILLGLVAHFGQWTKFDSRKTSLEDFYLDERTVR 240
 Db 181 NNWVQAMQKGLARSTKEIPDEISILLGLVAHFGQWTKFDSRKTSLEDFYLDERTVR 240

QY 241 VPMMSDPKAVLYGLSDLSCKIAQLPTGSMSTIFFLPKVTQNLTLIEESLTSBFIHD 300
 Db 241 VPMMSDPKAVLYGLSDLSCKIAQLPTGSMSTIFFLPKVTQNLTLIEESLTSBFIHD 300
 QY 301 IDRELKTVQAVLTVPKLKLSEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTVQAVLTVPKLKLSEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 QY 361 GFEWNEGAGTTPSPGLQPAHLTPFLDYHLNQPFIFVLRDITDGTGALLFIGKILDPGRP 418
 Db 361 GFEWNEGAGTTPSPGLQPAHLTPFLDYHLNQPFIFVLRDITDGTGALLFIGKILDPGRP 418

RESULT 8
 ABG72122
 ID ABG72122 standard; protein; 418 AA.
 XX
 AC ABG72122;
 DT 30-JAN-2003 (first entry)
 XX
 DE Human pigmented epithelium derived neurotrophic factor (PEDF).
 XX
 KW Human; retinal pigmented epithelium derived neurotrophic factor; PEDF;
 KW retinal disease; retinal tumour; retinoblastoma; retinal detachment;
 KW neuronal-retinal tumour; macular degeneration; retinitis pigmentosa;
 KW diabetic retinopathy; inherited and age-related pathology; tumour;
 KW ocular disease; nerve injury; serine protease related disorder;
 KW cystostatic; ophthalmological; antiinflammatory; antidiabetic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label= Signal_peptide
 FT # /label= Mature_PEDF
 XX
 FN US6451763-B1.
 XX
 PD 17-SEP-2002.
 XX
 XX 29-AUG-1995; 95US-00520373.
 XX
 PR 04-JUN-1992; 92US-00894215.
 PR 24-SEP-1992; 92US-00952796.
 PR 25-JUL-1994; 94US-00279979.
 PR 25-JAN-1995; 95US-00377710.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tombran-Tink J, Chader GU, Becerra SP, Rodriguez IR, Steele FR;
 PI Johnson LV;
 XX
 DR WPI: 2003-056723/05.
 DR N-PSDB; ABS57266.
 XX
 FT Treating retinal disease such as retinal tumors, retinitis pigmentosa,
 FT macular degeneration and diabetic retinopathy, in a subject, involves
 FT administering Pigment Epithelium Derived Factor to the subject.
 XX
 PS Claim 1; Col 61-64; 53pp; English.
 XX
 CC The present invention relates to the isolation of a human retinal
 CC pigmented epithelium derived neurotrophic factor (PEDF), and
 CC polynucleotide sequences encoding it. The gene encoding human PEDF maps
 CC to chromosome 17p13.1-pter. The invention also describes a truncated
 CC version of PEDF referred to as PEDF-BH, vectors comprising nucleic acids
 CC encoding PEDF or PEDF-BH, and a method of using these sequences to treat
 CC retinal diseases such as retinal tumours (e.g. retinoblastoma), neuronal-
 CC retinal tumours, macular degeneration, retinitis pigmentosa, retinal
 CC detachment, diabetic retinopathy, inherited and age-related pathologies,
 CC tumours, ocular diseases, nerve injuries, and conditions resulting from

CC the activity of serine proteases. The present sequence represents human
 CC PEDF
 SQ Sequence 418 AA;
 Query Match 98.4%; Score 2097; DB 6; Length 418;
 Best Local Similarity 98.8%; Pred. No. 1.3e-186;
 Matches 413; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MQALVLLLCIGALLGHSRCQNPASPPPEGSPDPSTGALVEEDPPFFKVPVKNLAAAVSN 60
 Db 1 MQALVLLLCIGALLGHSRCQNPASPPPEGSPDPSTGALVEEDPPFFKVPVKNLAAAVSN 60
 QY 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAERTESIIRALYYDLTSSPDHIG 120
 Db 61 FGVDLYRVRSSMPTTNVLLSPLSVATALSALSGAERTESIIRALYYDLTSSPDHIG 120
 QY 121 TYKELLDTVTAPQKNLKSASRIVFEKKLRIRKSSVAPLEKSYGTRPRVLTGNPRLDLOEI 180
 Db 121 TYKELLDTVTAPQKNLKSASRIVFEKKLRIRKSSVAPLEKSYGTRPRVLTGNPRLDLOEI 180
 QY 181 NNWQAOQMGKLABSTKEIPDEISILLGVAFHFGQVTKTDSRKTSLIEDFYLDEERTVR 240
 Db 181 NNWQAOQMGKLABSTKEIPDEISILLGVAFHFGVTKFDSRKTSLIEDFYLDEERTVR 240
 QY 241 VPMMSDPKAVLYGLSDLSCKIAQLPTGSMSTIFFLPKVTQNLTLIEESLTSBFIHD 300
 Db 241 VPMMSDPKAVLYGLSDLSCKIAQLPTGSMSTIFFLPKVTQNLTLIEESLTSBFIHD 300
 QY 301 IDRELKTVQAVLTVPKLKLSEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 Db 301 IDRELKTVQAVLTVPKLKLSEGEVTKSLQEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
 QY 361 GFEWNEGAGTTPSPGLQPAHLTPFLDYHLNQPFIFVLRDITDGTGALLFIGKILDPGRP 418
 Db 361 GFEWNEGAGTTPSPGLQPAHLTPFLDYHLNQPFIFVLRDITDGTGALLFIGKILDPGRP 418

RESULT 9
 ADB9089
 ID ADB9089 standard; protein; 418 AA.
 XX
 AC ADB9089;
 DT 04-DEC-2003 (first entry)
 DE Human retinal pigment epithelial-derived factor (PEDF).
 XX
 KW Human; retinal pigment epithelial-derived neurotrophic factor; PEDF;
 KW tumour; ocular disease; neuronal cell pathology; serine protease;
 KW blood coagulation; thrombosis; bacterial infection; parasitic infection;
 KW elastosis; vascular disorder; fibrinoid formation; coagulation disorder;
 KW arteriosclerosis; ischaemia; arthroses diabetes; emphysema; arthritis;
 KW septic shock; lung disease; complement activation; ulcer;
 KW ulcerative colitis; pancreatitis; psoriasis; fibrinolytic disease;
 KW arthropathy; bone resorption; hypertension; congestive heart failure;
 KW cirrhosis; protease allergy; chromosome 17p13.1-pter.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /note= "Signal peptide"
 FT Protein /note= "Mature PEDF"
 XX
 FN US2003096750-A1.
 XX 22-MAY-2003.
 PF 09-AUG-2002; 2002US-00216373.
 XX 04-JUN-1992; 92US-00894215.

PR 24-SEP-1992; 92US-00952796.
PR 29-AUG-1995; 95US-00520373.
XX (TOMB/) TOMBRAN-TINK J.
FA (STEE/) STEELE F R.
FA (CHAD/) CHADER G J.
FA (BECER/) BECERRA S P.
FA (JOHN/) JOHNSON L V.
FA (RODR/) RODRIGUEZ I R.
XX
PI Tombran-Tink J, Steele FR, Chader GJ, Becerra SP, Johnson LV;
PI Rodriguez IR;
XX
XX WPI; 2003-743982/70.
DR N-PSDB; ADB99088.
XX
XX New purified retinal pigmented epithelium derived neurotrophic factor
PT composition, useful for treating tumors, i.e. retinal tumor, ocular
PT disease, neuronal cell pathologies, coagulation disorders or
PT arteriosclerosis.
XX
XX Claim 3; SEQ ID NO 2; 58pp; English.
XX
XX The invention relates to a composition comprising purified retinal
CC pigmented epithelium derived neurotrophic factor (PEDF). The PEDF
CC proteins comprise ADB99089, ADB99090 or sequences equivalent to but not
CC identical to ADB99089. Human PEDF is encoded by ADB99088. Also included
CC are purifying PEDF, producing PEDF comprising expressing the DNA sequence
CC encoding the PEDF in a host cell, a recombinant DNA molecule comprising a
CC genomic DNA fragment for PEDF (appearing as ADB99091 - ADB99093), a
CC vector comprising a PEDF nucleic acid molecule, an organism transformed
CC with a recombinant DNA molecule comprising a retinal PEDF cDNA, a host
CC cell containing the vector, a recombinantly produced PEDF protein which
CC is free from the risks normally associated with proteins isolated or
CC purified from a naturally occurring source organism and a purified human
CC genomic DNA molecule encoding a PEDF protein. The purified retinal
CC pigmented epithelium derived neurotrophic factor is useful for treating
CC tumors, i.e. retinal tumor, ocular disease, neuronal cell pathologies,
CC or conditions resulting from the activity of serine proteases, e.g.
CC excessive or unwanted blood coagulation, thrombosis, bacterial infection,
CC parasitic infection, elastosis, vascular disorders involving fibrinoid
CC formation, coagulation disorders, arteriosclerosis, ischaemia, arthroses
CC diabetes, emphysema, arthritis, septic shock, lung diseases, excessive
CC complement activation, ulcers, ulcerative colitis, pancreatitis,
CC psoriasis, fibrinolytic disease, arthropathy, bone resorption,
CC hypertension, congestive heart failure, cirrhosis, or allergy caused by
CC proteases. The present sequence represents human retinal pigmented
CC epithelium derived neurotrophic factor (PEDF).
XX
SQ Sequence 418 AA;

Query Match 98.4%; Score 2097; DB 7; Length 418;
Best Local Similarity 98.8%; Pred. No. 1.3e-186;
Matches 413; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MQALVLLICIGALLGHSCQNFASPPREGSDPDSTGALVEEDPPFKVPVKLAASVN 60
DB 1 MQALVLLICIGALLGHSCQNFASPPREGSDPDSTGALVEEDPPFKVPVKLAASVN 60
QY 61 FGVDLYRVRSMSPPTNVLLSPLSVATALSALSILGAEQRTESIHRALYDLISSPDING 120
DB 61 FGVDLYRVRSMSPPTNVLLSPLSVATALSALSILGAEQRTESIHRALYDLISSPDING 120
QY 121 TYKELDDTVAPQKNLKSASRIVEFKLRIKSSVAPLEKSYGTRPRVLGNPRLDLOEI 180
DB 121 TYKELDDTVAPQKNLKSASRIVEFKLRIKSSVAPLEKSYGTRPRVLGNPRLDLOEI 180
QY 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHFGQWVTKFSDSKTSLEDFYLDERTVR 240
DB 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAFHFGHVSVTKFSDSKTSLEDFYLDERTVR 240
QY 241 VPWMSDPKAVLYRGDLSCKIAQLPLTGRMSIIFFLPKVTQNLTLIEESLTSEFIHD 300

DB 241 VPWMSDPKAVLYRGDLSCKIAQLPLTGRMSIIFFLPKVTQNLTLIEESLTSEFIHD 300
QY 301 IDRELKTVQAVLTVPKILSVGEVTKSLQEMKLOSLEDSDFSKITGKPIKLTQVEHRA 360
DB 301 IDRELKTVQAVLTVPKILSVGEVTKSLQEMKLOSLEDSDFSKITGKPIKLTQVEHRA 360
QY 361 GFENWEDGAGTTSPGLOPAHLTFFLDYHLNPFIFVLRTDTGALLFGIKLDPRGP 418
DB 361 GFENWEDGAGTTSPGLOPAHLTFFLDYHLNPFIFVLRTDTGALLFGIKLDPRGP 418

RESULT 10
AAR90288

ID AAR90288 standard; protein; 379 AA.

XX AAR90288;

DT 16-JAN-1997 (first entry)

DE Modified pigment epithelium-derived factor (rPEDF).

XX Pigment epithelium-derived factor; PEDF; neuronal cells; neurons;
KW glial cells; gliastatic; gliosis; central nervous system; CNS;
KW neurodegenerative disease; injury; neurotrophic; brain cells;
KW Parkinson's disease; photoreceptor cells; retina; inhibition;
KW proliferation; immunoassay; antibody; ageing; degenerative disease.
XX
OS Homo sapiens.
PN W09533480-A1.
PD 14-DEC-1995.
PF 06-JUN-1995; 95WO-US007201.
PR 07-JUN-1994; 94US-00257963.
PR 30-DEC-1994; 94US-00367841.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Chader GJ, Becerra SP, Schwartz JP, Taniwaki T;

WPI; 1996-039966/04.

XX Use of pigment epithelium derived factor - for enhancing neuronal cell
PT survival and inhibiting glial cell proliferation, useful, e.g. in CNS
PT cell culture or to treat neuro-degenerative diseases.

XX Disclosure; Page 66-67; 15pp; English.

XX Pigment epithelium-derived factor (PEDF) has both neurotrophic and
CC gliastatic activity, making it useful in cases where neurons die quickly
CC and glia tend to proliferate (gliosis), e.g. in CNS cell culture, in
CC neurodegenerative diseases and in CNS injury. The neurotrophic effect
CC of PEDF is especially useful for enhancing survival of neuronal cell
CC cultures intended for use in transplantation. These include cultures of
CC human foetal brain cells and neural retina and photoreceptor cells. The
CC gliastatic activity of PEDF can be applied to inhibiting glial cell
CC proliferation in certain tumors. Antibodies directed against PEDF can be
CC used for inhibiting PEDF activity or in an immunoassay for determining
CC levels of PEDF in fluid, cellular or tissue samples e.g. for determining
CC ageing and/or other degenerative diseases. This sequence is designated
CC rPEDF and comprises the amino acid sequence Met-Asn-Arg-Ile fused to
CC Asp44-Pro418 of PEDF

XX Sequence 379 AA;

Query Match 89.3%; Score 1904; DB 2; Length 379;
Best Local Similarity 99.7%; Pred. No. 1.2e-168;
Matches 374; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 44 DFFKVPVKLAASVNFQDLYRVRSSMSPPTNVLLSPLSVATALSALSILGAEQRTESI 103

Db 5 DPFKVPVKNKLAASVNFYDLYVRSSMSPTTNVLLSPISVATLSALSIGAEQRTESI 64
 QY 104 IHRALYDYLSSPDHGTGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 163
 Db 65 IHRALYDYLSSPDHGTGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 124
 QY 164 TRPVLGNPRDLQEIINNWWQAQMGKGLARSTKEIPDEISILLGVVAHFKGQWTKFDS 223
 Db 125 TRPVLGNPRDLQEIINNWWQAQMGKGLARSTKEIPDEISILLGVVAHFKGQWTKFDS 184
 QY 224 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVT 283
 Db 185 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVT 244
 QY 284 QNLTLIEESLTSEFIHDIIDRELKTQVAVLTVPKLSYEGETVTKSLQEMKLSLFDSPDF 343
 Db 245 QNLTLIEESLTSEFIHDIIDRELKTQVAVLTVPKLSYEGETVTKSLQEMKLSLFDSPDF 304
 QY 344 SKITGKPIKLTQVEHFRAGFEWNEAGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 403
 Db 305 SKITGKPIKLTQVEHFRAGFEWNEAGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 364
 QY 404 GALLFIGKILDPRGP 418
 Db 365 GALLFIGKILDPRGP 379
 RESULT 11
 ABG72123
 ID ABG72123 standard; protein; 379 AA.
 XX
 AC ABG72123;
 DT 30-JAN-2003 (first entry)
 XX
 DE Truncated version of human PEDF, PEDF-BH.
 KW Human; retinal pigmented epithelium derived neurotrophic factor; PEDF;
 KW retinal disease; retinal tumour; retinoblastoma; retinal detachment;
 KW neuronal retinal tumour; macular degeneration; retinitis pigmentosa;
 KW diabetic retinopathy; inherited and age-related pathology; tumour;
 KW ocular disease; nerve injury; serine protease related disorder;
 KW cystostatic; ophthalmological; antiinflammatory; antidiabetic; mutant;
 KW mutein; PEDF-BH.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..4
 FT /note= "N-terminal fusion peptide"
 FT Region 5..379
 FT /note= "Corresponds to amino acid residues 44-418 of
 FT human PEDF (ABG72122)"
 XX
 PN US6451763-B1.
 XX
 PD 17-SEP-2002.
 XX
 PF 29-AUG-1995; 95US-00520373.
 XX
 PR 04-JUN-1992; 92US-00894215.
 PR 24-SEP-1992; 92US-00952796.
 PR 25-JUL-1994; 94US-00279979.
 PR 25-JAN-1995; 95US-00377710.
 XX
 XX (USSS) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tombran-Tink J, Chader GJ, Becerra SP, Rodriguez IR, Steele PR;
 PI Johnson LV;
 XX
 DR WPI; 2003-056723/05.
 XX

PT Treating retinal disease such as retinal tumors, retinitis pigmentosa,
 PT macular degeneration and diabetic retinopathy, in a subject, involves
 XX administering Pigment Epithelium Derived Factor to the subject.
 PS Claim 1; Col 65; 53pp; English.
 XX
 CC The present invention relates to the isolation of a human retinal
 CC pigmented epithelium derived neurotrophic factor (PEDF), and
 CC polynucleotide sequences encoding it. The gene encoding human PEDF maps
 CC to chromosome 17p13.1-pter. The invention also describes a truncated
 CC version of PEDF referred to as PEDF-BH, vectors comprising nucleic acids
 CC encoding PEDF or PEDF-BH, and a method of using these sequences to treat
 CC retinal diseases such as retinal tumours (e.g. retinoblastoma), neuronal -
 CC retinal tumours, macular degeneration, retinitis pigmentosa, retinal
 CC detachment, diabetic retinopathy, inherited and age-related pathologies,
 CC tumours, ocular diseases, nerve injuries, and conditions resulting from
 CC the activity of serine proteases. The present sequence represents human
 CC PEDF-BH which has an N-terminal fusion to Asp44-Pro418 of human PEDF
 CC (ABG72122), such that Met1-Glu43 of human PEDF are deleted in this
 CC version
 XX
 SQ Sequence 379 AA;
 Query Match 87.8%; Score 1870; DB 6; Length 379;
 Best Local Similarity 98.7%; Pred. No. 1.8e-165;
 Matches 370; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 44 DPFKVPVKNKLAASVNFYDLYVRSSMSPTTNVLLSPISVATLSALSIGAEQRTESI 103
 Db 5 DPFKVPVKNKLAASVNFYDLYVRSSMSPTTNVLLSPISVATLSALSIGAEQRTESI 64
 QY 104 IHRALYDYLSSPDHGTGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 163
 Db 65 IHRALYDYLSSPDHGTGTYKELLDTVTAPQNLKASRIVFEEKLRKSSFVAPLEKSYG 124
 QY 164 TRPVLGNPRDLQEIINNWWQAQMGKGLARSTKEIPDEISILLGVVAHFKGQWTKFDS 223
 Db 125 TRPVLGNPRDLQEIINNWWQAQMGKGLARSTKEIPDEISILLGVVAHFKGQWTKFDS 184
 QY 224 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVT 283
 Db 185 RKTSLDFYLDERTVRVPMMSDPKAVLRVGLSDLSCKIAQLPLTGSMIIIFFLPKVT 244
 QY 284 QNLTLIEESLTSEFIHDIIDRELKTQVAVLTVPKLSYEGETVTKSLQEMKLSLFDSPDF 343
 Db 245 QNLTLIEESLTSEFIHDIIDRELKTQVAVLTVPKLSYEGETVTKSLQEMKLSLFDSPDF 304
 QY 344 SKITGKPIKLTQVEHFRAGFEWNEAGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 403
 Db 305 SKITGKPIKLTQVEHFRAGFEWNEAGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRTDT 364
 QY 404 GALLFIGKILDPRGP 418
 Db 365 GALLFIGKILDPRGP 379
 RESULT 12
 ADB99090
 ID ADB99090 standard; protein; 379 AA.
 XX
 AC ADB99090;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human retinal pigment epithelial-derived factor, PEDF-BH.
 XX
 KW Human; retinal pigment epithelial-derived neurotrophic factor; PEDF-BH;
 KW tumour; ocular disease; neuronal cell pathology; serine protease;
 KW blood coagulation; thrombosis; bacterial infection; parasitic infection;
 KW elastosis; vascular disorder; fibroid formation; coagulation disorder;
 KW arteriosclerosis; ischaemia; arthrosis diabetes; emphysema; arthritis;
 KW septic shock; lung disease; complement activation; ulcer;
 KW ulcerative colitis; pancreatitis; psoriasis; fibrinolytic disease;

KW arthropathy; bone resorption; hypertension; congestive heart failure;
 KW cirrhosis; protease allergy; chromosome 17p13.1-pter.
 XX Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..4
 FT /note= "Replaces amino acids 1-43 of the wild-type PEDF
 FT protein"
 XX
 XX US2003096750-A1.
 XX
 PD 22-MAY-2003.
 XX
 PF 09-AUG-2002; 2002US-00216373.
 XX
 PR 04-JUN-1992; 92US-00894215.
 PR 24-SEP-1992; 92US-00952796.
 PR 29-AUG-1995; 95US-00520373.
 XX
 XX (TOMB/) TOMBRAN-TINK J.
 PA (STEE/) STEELE F R.
 PA (CHAD/) CHADER G J.
 PA (BECE/) BECERRA S P.
 PA (JOHN/) JOHNSON L V.
 PA (RODR/) RODRIGUEZ I R.
 XX
 XX Tombran-Tink J, Steele FR, Chader GJ, Becerra SP, Johnson LV,
 PI Rodriguez IR;
 XX
 XX WPI; 2003-743982/70.
 XX
 FT New purified retinal pigmented epithelium derived neurotrophic factor
 FT composition, useful for treating tumors, i.e. retinal tumor, ocular
 FT disease, neuronal cell pathologies, coagulation disorders or
 FT arteriosclerosis.
 XX
 PS Claim 5; SEQ ID NO 3; 58pp; English.
 XX
 CC The invention relates to a composition comprising purified retinal
 CC pigmented epithelium derived neurotrophic factor (PEDF). The PEDF
 CC proteins comprise ADB99089, ADB99090 or sequences equivalent to but not
 CC identical to ADB99089. Human PEDF is encoded by ADB99088. Also included
 CC are purifying PEDF, producing PEDF comprising expressing the DNA sequence
 CC encoding the PEDF in a host cell, a recombinant DNA molecule comprising a
 CC genomic DNA fragment for PEDF (appearing as ADB99091 - ADB99093), a
 CC vector comprising a PEDF nucleic acid molecule, an organism transformed
 CC with a recombinant DNA molecule comprising a retinal PEDF cDNA, a host
 CC cell containing the vector, a recombinantly produced PEDF protein which
 CC is free from the risks normally associated with proteins isolated or
 CC purified from a naturally occurring source organism and a purified human
 CC genomic DNA molecule encoding a PEDF protein. The purified retinal
 CC pigmented epithelium derived neurotrophic factor is useful for treating
 CC tumors, i.e. retinal tumor, ocular disease, neuronal cell pathologies,
 CC or conditions resulting from the activity of serine proteases, e.g.
 CC excessive or unwanted blood coagulation, thrombosis, bacterial infection,
 CC parasitic infection, elastosis, vascular disorders involving fibrinoid
 CC formation, coagulation disorders, arteriosclerosis, ischaemia, atheros
 CC diabetes, emphysema, arthritis, septic shock, lung diseases, excessive
 CC complement activation, ulcers, ulcerative colitis, pancreatitis,
 CC porriasis, fibrinolytic disease, arthropathy, bone resorption,
 CC hypertension, congestive heart failure, cirrhosis, or allergy caused by
 CC proteases. The present sequence represents a human retinal pigmented
 CC epithelium derived neurotrophic factor PEDF-BH where amino acids 1-43 of
 CC wild-type PEDF has been replaced by Met-Asn-Arg-Ile-Asp.
 XX
 SQ Sequence 379 AA;
 Query Match 87.8%; Score 1870; DB 7; Length 379;
 Best Local Similarity 98.7%; Pred. No. 1.8e-165;
 Matches 370; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 44 DPFKVPVNVKLAASVNFYDLYRVRSSMPTTNVLLSPLSVATLSALSGLGAEQRTESI 103
 Db 5 DFFKVPVNVKLAASVNFYDLYRVRSSMPTTNVLLSPLSVATLSALSGLGAEQRTESI 64
 QY 104 IHRALYYDLISSPDHGTIKELLDVTAPQKVKASRIIVFEKKRIKSSFVAPLEKSYG 163
 Db 65 IHRALYYDLISSPDHGTIKELLDVTAPQKVKASRIIVFEKKRIKSSFVAPLEKSYG 124
 QY 164 TRPRVLTGNPRDLQEIINNVOAKMGKILARSTKIPDEISILLGLVAHFKGQWTKPDS 223
 Db 125 TRPRVLTGNPRDLQEIINNVOAKMGKILARSTKIPDEISILLGLVAHFKGQWTKPDS 184
 QY 224 RKTSLDFYLDERTVRVPMMSDPKAVRLRYGLDLSCKIAQLPTGSMISIFFPLKVT 283
 Db 185 RKTSLDFYLDERTVRVPMMSDPKAVRLRYGLDLSCKIAQLPTGSMISIFFPLKVT 244
 QY 284 QNLTIIEESLTSEFTHIDRELKTVQAVLTVPKLSYEGETVKSLQENKLSLQSLDFSPDF 343
 Db 245 QNLTIIEESLTSEFTHIDRELKTVQAVLTVPKLSYEGETVKSLQENKLSLQSLDFSPDF 304
 QY 344 SKITCKPIKLTQVEHRAQFEMNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRTDIT 403
 Db 305 SKITCKPIKLTQVEHRAQFEMNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRTDIT 364
 QY 404 GALLFIGKILDPRGP 418
 Db 365 GALLFIGKILDPRGP 379

RESULT 13
 ABB57391
 ID ABB57391 standard; protein; 418 AA.
 XX
 AC ABB57391;
 DT 07-AUG-2003 (revised)
 DT 08-MAR-2002 (first entry)
 XX
 DE Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 36.
 XX
 KW Rat; heart; cardiatic; myocardial necrosis; cardiac hypertrophy;
 KW cardiac insufficiency.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200183705-A1.
 PD 08-NOV-2001.
 PF 27-APR-2001; 2001WO-JP003700.
 PR 27-APR-2000; 2000JP-00126741.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Yamada Y, Sekine S, Kikuchi Y, Sakurada K;
 PI WPI: 2002-075160/10.
 DR N-PSDB; ABI99933.
 XX
 XX Genes having differential expression in fetal and adult heart tissue
 PT useful for screening potential drugs for promoting repair of damage
 PT caused by myocardial necrosis.
 XX
 PS Claim 53; Page 153-155; 171pp; Japanese.
 XX
 CC The invention relates to gene sequences (ABI99915-ABI99934) having
 CC modified expression in fetal heart tissue as compared to adult heart
 CC tissue and the encoded proteins (ABB57375-ABB57392). The genes have
 CC cardiatic activity and may be useful in the promotion of the repair of
 CC damage to heart tissue caused by myocardial necrosis. The gene sequences
 CC are useful for screening potential compounds for the ability to influence
 CC disease associated with myocardial necrosis. Drugs identified by the

CC screening methods may be used to treat and prevent disease with which
 CC myocardial necrosis is associated, such as cardiac hypertrophy and
 CC cardiac insufficiency. Diagnosis of diseases such as those above is also
 CC disclosed. (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 418 AA;

Query Match 84.0%; Score 1789; DB 5; Length 418;
 Best Local Similarity 83.5%; Pred. No. 7.5e-158;
 Matches 348; Conservative 36; Mismatches 29; Indels 4; Gaps 3;

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 Qy 59 SNFGYDLVYRVRSSMPTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDI 118
 Db 59 SNFGYDLVYLRSGAVSTGNILLSPLSVATALSALSGAEQRTESVHRALYYDLINPDI 118
 Qy 119 HGTYKELLDTVTAPOKNLKSASRIKSVFAPLEKSYGTRPRVLTCGNPRDLQ 178
 Db 119 HSTYKELLASVTAPEKNFKASRIKSVFAPLEKSYGTRPRILTCGNPRIDLQ 178
 Qy 179 EINNVOAQMKGLARSTKIPBISILLGVAFHGQWTKFDSKTSLEDFYLDERT 238
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 Db 239 VRVPMMSDPKAILRYGLDSDLNCKIAQLPLTGSMSIIFFLPKVTONLTIIESLTSEFI 298
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 Db 299 HDIDRELKTQAVLTVPKLSYEGEVTKLSQEMKLSLQSLFDSDFSKITGKPKLTQVEH 358
 Qy 359 RAGFEMNEDGAGTTPSGLOPAHLTPFLDYHLNQPFIFVLRTDTTGALLFIGKILDP 415
 Db 359 RAAEFMNEEGAGTSSNDLPQVLTPLDYHLNRPFIIFVLRTDTTGALLFIGKILDP 415

RESULT 14

AAW97364
 ID AAW97364 standard; peptide; 362 AA.

XX AC AAW97364;

XX DT 12-MAY-1999 (first entry)

XX DE Amino acid sequence of SLED (an antiangiogenic protein).

XX KW SLED; antiangiogenic protein; angiogenesis; endothelial cell migration;
 XX KW hair growth; tumour growth; angiogenic disease; reproduction;
 XX KW tumour prognosis; angiogenesis-related disorder.

XX OS Unidentified.

XX PN WO9904806-A1.

XX PD 04-FEB-1999.

XX PF 23-JUL-1998; 98WO-US015228.

XX PR 23-JUL-1997; 97US-00899304.

XX PA (NOUN) UNIV NORTHWESTERN.

XX PI Bouck NP, Dawson DW, Gillis PR;

XX XX WPI; 1999-142603/12.

XX XX Inhibiting endothelial cell migration and angiogenesis within a tissue -
 XX FT by providing exogenous SLED, useful to treat angiogenic diseases, and
 XX FT assess tumour severity.

XX Disclosure; Page 25-26; 28pp; English.

XX The present sequence represents SLED, an antiangiogenic protein.
 CC Angiogenesis within a tissue can be inhibited by providing exogenous SLED
 CC to endothelial cells associated with the tissue. Exogenous SLED can also
 CC be used to inhibit endothelial cell migration, stimulate hair growth, to
 CC inhibit tumour growth. It can also be used for determining the severity
 CC of a tumour, wherein absence of SLED within the tumour indicates an
 CC advanced state, and presence of SLED indicates an early state of the
 CC tumour. The invention is used in the treatment of angiogenic diseases, to
 CC interfere with angiogenesis associated with reproductive functions, to
 CC assess the prognosis of tumours and other angiogenesis-related disorders,
 CC and to investigate angiogenesis in vitro

XX SQ Sequence 362 AA;

Query Match 83.7%; Score 1784; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.8e-157;
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 Db 121 TYKELLDTVTAPOKNLKSASRIKSVFAPLEKSYGTRPRVLTCGNPRDLQEI 180
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 Db 301 IDRELKTQAVLTVPKLSYEGEVTKLSQEMKLSLQSLFDSDFSKITGKPKLTQ 355

RESULT 15

AAU08652
 ID AAU08652 standard; protein; 362 AA.

XX AC AAU08652;

XX DT 18-DEC-2001 (first entry)

XX DE Human antiangiogenic protein SLED.

XX KW Human; SLED; antiangiogenic; antiinflammatory; antiarteriosclerotic;
 KW dermatological; antidiabetic; antipsoriatic; antiarthritic; vasotropic;
 KW ophthalmological; gynecological; cytostatic; tumour; psoriasis;
 KW scleroderma; neovascularisation; bacterial ulceration; muscle disease;
 KW intestinal adhesion; Crohn's disease; atherosclerosis; scleroderma;
 KW hypertrophic scar; eye injury; hypoxia; infection; diabetes;
 KW retinoblastoma; birth control.

XX OS Homo sapiens.

XX XX Key Location/Qualifiers

XX FT Peptide 1..20

XX FT /label= Signal_peptide

XX FT Protein 21..362

XX FT /label= Mature_SLED

XX FT Region 44..157

XX FT /label= Active_fragment

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Search completed: September 1, 2004, 11:14:59
Job time : 131 secs

FT Region /note= "Region displaying SLED activity"
FT 45..121
FT /label= Active fragment
XX /note= "Region displaying SLED activity"
XX
FN US6288024-B1.
XX
XX 11-SEP-2001.
XX
XX 23-JUL-1998; 98US-00122079.
XX
XX 23-JUL-1997; 97US-00899304.
XX
XX (NOUN) UNIV NORTHWESTERN.
XX
XX Bouck NP, Dawson DW, Gillis PR;
XX WPI; 2001-579337/65.
XX
XX Inhibition of angiogenesis/endothelial cell migration within a tissue
PT involves providing exogenous antiangiogenic protein to endothelial cells
PT associated with the tissue.
PT
XX Disclosure; Col 12-14; 17pp; English.
XX
XX The invention relates to inhibition of angiogenesis/endothelial cell
CC migration within a tissue involving providing exogenous antiangiogenic
CC protein (SLED) to endothelial cells associated with the tissue. The
CC method is used for treating a host of diseases associated with
CC angiogenesis and for interfering with angiogenesis associated with
CC reproductive functions, for assessing the prognosis of tumours, useful
CC reagents for investigation of angiogenesis, for treating diseases and
CC disorders such as psoriasis, scleroderma, tumours of the skin,
CC neovascularisation as a consequence of infection like cat scratch
CC disease, bacterial ulceration or other skin disorders, blood vessels,
CC muscle diseases, joints, for treating disorders associated with
CC stimulation of endothelial cell migration such as intestinal adhesion,
CC Crohn's disease, atherosclerosis, scleroderma and hypertrophic scars, for
CC treating eye injury, hypoxia, infection, surgery, laser surgery,
CC diabetes, retinoblastoma or other diseases or disorders of the eye, to
CC modulate or prevent the occurrence of normal physiological conditions
CC associated with neovascularisation, can be used as a birth control,
CC attenuated neovascularisation associated with ovulation, implantation of
CC an embryo and placenta formation. The present sequence is human SLED
XX
SQ Sequence 362 AA;

Query Match 83.7%; Score 1784; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.8e-157;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEEDPFFKVPVNKLAASN 60
Db 1 MQALVLLLCIGALLGHSSCONPASPPEGSPDPDSTGALVEEEDPFFKVPVNKLAASN 60

Qy 61 FGVDLYVRSMPTTNVLLSPLSVATALSALSGAEQRTESIIRALYYDLISSPDH 120
Db 61 FGVDLYVRSMPTTNVLLSPLSVATALSALSGAEQRTESIIRALYYDLISSPDH 120

Qy 121 TYKELDTVTAPQKNLSASRIYFEKKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQEI 180
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 11:15:04 ; Search time 51 Seconds
(without alignments)

2578.592 Million cell updates/sec

Title: US-10-619-149-1

Perfect score: 2131

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Scoring table: BLOSUM62

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Searched: 1297172 seqs, 314612898 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2125	99.7	418	14	Sequence 1, Appli
4	2125	99.7	418	15	Sequence 1, Appli
5	2125	99.7	418	15	Sequence 1, Appli
6	2106	98.8	418	12	Sequence 34, Appl
7	2097	98.4	418	14	Sequence 2, Appli
8	1870	87.8	379	14	Sequence 3, Appli
9	1789	84.0	418	15	Sequence 36, Appl
10	1784	83.7	362	9	Sequence 1, Appli
11	538.5	25.3	360	12	Sequence 67, Appl
12	538.5	25.3	360	15	Sequence 88, Appl
13	499	23.4	125	14	Sequence 84, Appl
14	458.5	21.5	377	10	Sequence 31, Appl
15	453.5	21.3	377	12	Sequence 66, Appl

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16 453 21.3 371 15 US-10-023-634-87 Sequence 87, Appl
17 444 20.8 413 16 US-10-470-390A-38 Sequence 38, Appl
18 443 20.8 403 14 US-10-316-253-36 Sequence 36, Appl
19 432.5 20.3 503 14 US-10-025-514-8 Sequence 8, Appl
20 431 20.2 418 16 US-10-408-765A-2304 Sequence 2304, Ap
21 430 20.2 417 14 US-10-308-279-26 Sequence 26, Appl
22 430 20.2 417 16 US-10-624-631-23 Sequence 23, Appl
23 429 20.1 418 10 US-09-992-600A-92 Sequence 92, Appl
24 429 20.1 418 10 US-09-992-340-92 Sequence 92, Appl
25 429 20.1 418 10 US-09-992-095B-92 Sequence 92, Appl
26 429 20.1 418 10 US-09-999-570-92 Sequence 92, Appl
27 429 20.1 418 14 US-10-000-489-92 Sequence 92, Appl
28 429 20.1 418 14 US-10-000-986-92 Sequence 92, Appl
29 429 20.1 418 14 US-10-154-678-92 Sequence 92, Appl
30 427 20.0 418 12 US-10-411-037-22 Sequence 22, Appl
31 427 20.0 418 12 US-10-411-026-22 Sequence 22, Appl
32 427 20.0 418 14 US-10-097-340-286 Sequence 286, App
33 427 20.0 418 16 US-10-410-962-22 Sequence 22, Appl
34 427 20.0 418 16 US-10-411-049-22 Sequence 22, Appl
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40 426 20.0 522 14 US-10-025-514-14 Sequence 14, Appl
41 424 19.9 418 16 US-10-408-765A-54 Sequence 54, Appl
42 421 19.8 394 10 US-09-993-180-6 Sequence 6, Appl
43 421 19.8 394 14 US-10-025-514-2 Sequence 2, Appl
44 421 19.8 503 14 US-10-025-514-16 Sequence 16, Appl
45 421 19.8 522 14 US-10-025-514-20 Sequence 20, Appl
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ALIGNMENTS

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; Sequence 1, Application US/10619149
; Publication NO. US20040161423A1
; GENERAL INFORMATION:
; APPLICANT: Valentis, Inc.
; APPLICANT: Kumar, Sanjeev M
; TITLE OF INVENTION: Polymer Modified Anti-Angiogenic Serpins
; FILE REFERENCE: 213-0086US
; CURRENT APPLICATION NUMBER: US/10/619,149
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,786
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 418
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Human PEDF
; LOCATION: (1)..(418)
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; NAME/KEY: predicted signal sequence
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; OTHER INFORMATION: Cleavage site might be C or Q
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; NAME/KEY: Predicted mature polypeptide
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; FEATURE:
; NAME/KEY: predicted neurotropic activity and receptor binding
; LOCATION: (68)..(121)
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; NAME/KEY: collagen binding domain
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RESULT 4
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; Sequence 1, Application US/10342243
; Publication No. US20030216286A1
; GENERAL INFORMATION:
; APPLICANT: BOUCK, No. US20030216286A11
; APPLICANT: DAWSON, David
; APPLICANT: GILLIS, Paul
; APPLICANT: VOLPERT, Olga
; APPLICANT: CRAWFORD, Susan
; APPLICANT: STELLMACH, Veronica
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 053662-5018-00
; CURRENT APPLICATION NUMBER: US/10/342,243
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-342-243-1

Query Match 99.7%; Score 2125; DB 15; Length 418;
Best Local Similarity 99.5%; Pred. No. 3.2e-188;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1, Application US/10603387
; Publication No. US20040014664A1
; GENERAL INFORMATION:
; APPLICANT: BOUCK, No. US20040014664A11
; APPLICANT: DAWSON, David
; APPLICANT: GILLIS, Paul
; APPLICANT: VOLPERT, Olga
; APPLICANT: CRAWFORD, Susan
; APPLICANT: STELLMACH, Veronica
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 053662-5018-00
; CURRENT APPLICATION NUMBER: US/10/603,387
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-603-387-1

Query Match 99.7%; Score 2125; DB 15; Length 418;
Best Local Similarity 99.5%; Pred. No. 3.2e-188;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQALVLLCIGALLGHSSCONPASPPEEGSPDPDSTGALVEEEDPPFKVPVKNKLAASN 60
Db 1 MQALVLLCIGALLGHSSCONPASPPEEGSPDPDSTGALVEEEDPPFKVPVKNKLAASN 60
Qy 61 FGVDLYRVRSSMSTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDING 120
Db 61 FGVDLYRVRSSMSTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDING 120
Qy 121 TYKELLDTVTAPQKNLKSASRIVPEKLRKSSFVAPLEKSYGTRPVLGTGNPRDLQEI 180
Db 121 TYKELLDTVTAPQKNLKSASRIVPEKLRKSSFVAPLEKSYGTRPVLGTGNPRDLQEI 180
Qy 181 NNWVQAMKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLSEDFYLDERTVR 240
Db 181 NNWVQAMKGLARSTKEIPDEISILLGVAFHKGQWTVKFSRKTSLSEDFYLDERTVR 240
Qy 241 VPMMSDPKAVLYRGDSDLSCKIAQLPLTGSMSIIFPLPKVTQNLTLIEESLTSFIHD 300
Db 241 VPMMSDPKAVLYRGDSDLSCKIAQLPLTGSMSIIFPLPKVTQNLTLIEESLTSFIHD 300
Qy 301 IDRELKTQVAVLTVPKLSYEGSVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTQVAVLTVPKLSYEGSVTKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
Qy 361 GFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418
Db 361 GFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDITDGTGALLFIGKILDRPGP 418

RESULT 6
US-10-262-839-34
; Sequence 34, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,

APPLICANT: Boldog, Ferenc,
APPLICANT: Burgess, Catherine,
APPLICANT: Catterton, Elina,
APPLICANT: Edinger, Shlomit,
APPLICANT: Ellerman, Karen,
APPLICANT: Gerlach, Valerie,
APPLICANT: Gorman, Linda,
APPLICANT: Guo, Xiaolia,
APPLICANT: Ji, Weizhen,
APPLICANT: Kekuda, Rameeh,
APPLICANT: Leach, Martin,
APPLICANT: Li, Li,
APPLICANT: Miller, Charles,
APPLICANT: Patturajan, Meera,
APPLICANT: Reiger, Daniel,
APPLICANT: Rothenberg, Mark,
APPLICANT: Shimkets, Richard,
APPLICANT: Smithson, Glenda,
APPLICANT: Spytek, Kimberly,
APPLICANT: Taupier, Raymond, Jr.,
APPLICANT: Vernet, Corine,
APPLICANT: Voss, Edward,
APPLICANT: Zerhusen, Brian,
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-462A
CURRENT APPLICATION NUMBER: US/10/262,839
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,044
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,849
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/374,738
PRIOR FILING DATE: 2002-04-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 367
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 34
LENGTH: 418
TYPE: EXT
ORGANISM: Homo sapiens
US-10-262-839-34
Query Match 98.8%; Score 2106; DB 12; Length 418;
Best Local Similarity 99.0%; Pred. No. 1.8e-186;
Matches 414; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MQALVLLCTGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKNKLAASVN 60
Db 1 MQALVLLCTGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKNKLAASVN 60
Qy 61 FGDLVVRSSMSTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDH 120
Db 61 FGDLVVRSSMSTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDH 120
Qy 121 TYKELLDTVTAPQKNLSASRIVEKKLRKSSVFAPLEKSYGTRPRVLTGNPRDLQEI 180
Db 121 TYKELLDTVTAPQKNLSASRIVEKKLRKSSVFAPLEKSYGTRPRVLTGNPRDLQEI 180

Qy 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAHFQGVTKFDSRKTSLSEFYLDEERTVR 240
Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAHFQGVTKFDSRKTSLSEFYLDEERTVR 240
Qy 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIESLTSSEIHD 300
Db 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIESLTSSEIHD 300
Qy 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLQSLFSDPFSKTKTGKPKLTQVSHRA 360
Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSLQSLFSDPFSKTKTGKPKLTQVSHRA 360
Qy 361 GFENEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFIKILDPGCP 418
Db 361 GFENEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFIKILDPGCP 418
RESULT 7
US-10-216-373-2
Sequence 2, Application US/10216373
Publication No. US20030096750A1
GENERAL INFORMATION:
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
APPLICANT: Rodriguez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
FILE REFERENCE: 2026-4203US1
CURRENT APPLICATION NUMBER: US/10/216,373
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/08/520,373
PRIOR FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 418
TYPE: PRT
ORGANISM: HUMAN
US-10-216-373-2
Query Match 98.4%; Score 2097; DB 14; Length 418;
Best Local Similarity 98.8%; Pred. No. 1.3e-185;
Matches 413; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MQALVLLCTGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKNKLAASVN 60
Db 1 MQALVLLCTGALGHSCQNPASPPPEGSPDPDSTGALVEEDPPFKVPVKNKLAASVN 60
Qy 61 FGDLVVRSSMSTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDH 120
Db 61 FGDLVVRSSMSTTNVLLSPLSVATALSALSGAEQRTESIHRALYYDLISSPDH 120
Qy 121 TYKELLDTVTAPQKNLSASRIVEKKLRKSSVFAPLEKSYGTRPRVLTGNPRDLQEI 180
Db 121 TYKELLDTVTAPQKNLSASRIVEKKLRKSSVFAPLEKSYGTRPRVLTGNPRDLQEI 180
Qy 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAHFQGVTKFDSRKTSLSEFYLDEERTVR 240
Db 181 NNWVQAQMGKGLARSTKEIPDEISILLGVAHFQGVTKFDSRKTSLSEFYLDEERTVR 240
Qy 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIESLTSSEIHD 300
Db 241 VPMMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLKVTQNLTLIESLTSSEIHD 300

QY 301 IDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
DB 301 IDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFGKILDRGP 418
DB 361 GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFGKILDRGP 418

RESULT 8
US-10-216-373-3
; Sequence 3, Application US/10216373
; Publication No. US20030096750A1
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/10/216,373
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/08/520,373
; PRIOR FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: /note= Met 1...Ile 4 is an N-terminal fusion to
; OTHER INFORMATION: Asp 44...Pro 418 of SEQ ID No. US20030096750A1 2; Met 1...Glu 43
; OTHER INFORMATION: of SEQ ID NO:2 is deleted
US-10-216-373-3

Query Match 87.8%; Score 1870; DB 14; Length 379;
Best Local Similarity 99.7%; Pred. No. 1.3e-164;
Matches 370; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 44 DPFKVPVKNLAAAVSNFGDYLVRRSSMSPTTNVLLSPSLVATLSALSGAEQRTESI 103
DB 5 DFFKVPVKNLAAVSNFGKDYLVRRSSMSPTTNVLLSPSLVATLSALSGAEQRTESI 64
QY 104 IHRALYYDLISSPDHGTXYKELDTVTAPQKNLKSASRIVFEEKLRKSSFVAPLEKSYG 163
DB 65 IHRALYYDLISSPDHGTXYKELDTVTAPQKNLKSASRIVFEEKLRKSSFVAPLEKSYG 124
QY 164 TRPVLGNPRDLQEQINNVAQOMKGLARSTKEIPDEISILLGVAFKQGWTKFDS 223
DB 125 TRPVLGNPRDLQEQINNVAQOMKGLARSTKEIPDEISILLGVAFKQGWTKFDS 184
QY 224 RKTSLDFYLDERTVRPMMSPKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVT 283
DB 185 RKTSLDFYLDERTVRPMMSPKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVT 244
QY 284 QNLTILIEESLTSBFIHIDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDF 343
DB 245 QNLTILIEESLTSBFIHIDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDF 304
QY 344 SKITGPKIKLTQVEHRA GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDT 403

DB 305 SKITGPKIKLTQVEHRA GFENWEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDT 364
QY 404 GALLFIGKILDRGP 418
DB 365 GALLFIGKILDRGP 379
RESULT 9
US-10-258-666-36
; Sequence 36, Application US/10258666
; Publication No. US20040005578A1
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; APPLICANT: Sekine, Susumu
; APPLICANT: Kikuchi, Yasuhiro
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Kyowa Hakkō Kogyo Co., Ltd.
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
; FILE REFERENCE: 082382-000000US
; CURRENT APPLICATION NUMBER: US/10/258,666
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: JP 2000-126741
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: WO PCT/JPO1/03700
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: RHDH-140, PEDF
US-10-258-666-36

Query Match 84.0%; Score 1789; DB 15; Length 418;
Best Local Similarity 83.5%; Pred. No. 4.9e-157;
Matches 348; Conservative 36; Mismatches 29; Indels 4; Gaps 3;
QY 1 MQALVLLLCIGALLGHSSQON-PASPPBEGSPDPDSTG-ALVVEEDPPFKVPVKNLAAAV 58
DB 1 MOTLVLLLTGTGALLGHSSQNVFDS--SQDSPAPDSTGEPVVEEDPPFKVPVKNLAAAV 58
QY 59 SNFGDYLVRRSSMSPTTNVLLSPSLVATLSALSGAEQRTESIHRALYYDLISSPDI 118
DB 59 SNFGDYLVRRSGAVSTGNILLSPSLVATLSALSGAEQRTESVIHRALYYDLINPDI 118
QY 119 HGTXYKELDTVTAPQKNLKSASRIVFEEKLRKSSFVAPLEKSYGTRPRVLGTGNPRDLQ 178
DB 119 HSTYKELLASVTAPENKPKASRIVFEEKLRKSSFVAPLEKSYGTRPRITGNPRDLQ 178
QY 179 EINNVAQOMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLDERT 238
DB 179 EINNVAQOMKGLARSTREMPALSILLGVAFKQGWTKFDSRKTTLQDFHLDERT 238
QY 239 VRVPMSPKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPKVTQNLTLIEESLTSBFI 298
DB 239 VRVPMSPKAVLRYGLSDLSCKIAQLPLTGSMSIIFFLPKVTQNLTLIEESLTSBFI 298
QY 299 HDIDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEH 358
DB 299 HDIDRELKTQAVLTVPKLSYEGETVKSLOEMKLSLFDSPDFSKITGPKIKLTQVEH 358
QY 359 RAGFEWNEEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFIGKILDP 415
DB 359 RAAFEWNEEDGAGTTSSNPDIQPVRLTFPLDYHLNRPFIIVLRDTDTGALLFIGKILDP 415

RESULT 10
US-09-875-114-1
; Sequence 1, Application US/09875114
; Patent No. US2002002131A1
; GENERAL INFORMATION:

APPLICANT: No. US200200002131althwestern University
APPLICANT: No. US200200002131a11 Bouck
APPLICANT: David Dawson
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
FILE REFERENCE: 0290-2302
CURRENT APPLICATION NUMBER: US/09/875,114
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: US 08/899,304
PRIOR FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 362
TYPE: PRT
ORGANISM: Homo sapiens
US-09-875-114-1

Query Match 83.7%; Score 1784; DB 9; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.1e-156; Indels 0; Gaps 0;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQALVLLCTGALGHSSCONPSPPEEGSPDPSTGALVEEDDPFKVPVVKLAASVN 60
DB 1 MQALVLLCTGALGHSSCONPSPPEEGSPDPSTGALVEEDDPFKVPVVKLAASVN 60
QY 61 FGVDLYVRSSMPTTNVLLSPVSATLSALSGAEQRTESIHRALYDILISSPDH 120
DB 61 FGVDLYVRSSMPTTNVLLSPVSATLSALSGAEQRTESIHRALYDILISSPDH 120
QY 121 TYKELDTVTAPQKLSASRIVFEXKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQ 180
DB 121 TYKELDTVTAPQKLSASRIVFEXKLRKSSFVAPLEKSYGTRPRVLTGNPRDLQ 180
QY 181 NNWQVQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLBERTVR 240
DB 181 NNWQVQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLBERTVR 240
QY 241 VPWMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFFLPKVTQNTLIEESLTSEFIH 300
DB 241 VPWMSDPKAVLYRGDLSCKIAQLPLTGSMSIIFFLPKVTQNTLIEESLTSEFIH 300
QY 301 IDRELKTQVAVLTVPKLSYGEVTKSLQEMKLSLQSLFSDPSFKITGPKIKLTQ 355
DB 301 IDRELKTQVAVLTVPKLSYGEVTKSLQEMKLSLQSLFSDPSFKITGPKIKLTQ 355

RESULT 11

US-10-037-417-67
Sequence 67, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaochong
APPLICANT: Sytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciorra, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark

APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 67
LENGTH: 360
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Serpin
OTHER INFORMATION: Consensus Sequence
US-10-037-417-67

Query Match 25.3%; Score 538.5; DB 12; Length 360;
Best Local Similarity 33.6%; Pred. No. 4.7e-41;
Matches 122; Conservative 88; Mismatches 140; Indels 13; Gaps 9;
QY 63 YDLVVRSSMPTTNVLLSPVSATLSALSGAEQRTESIHRALYDIL--ISSPDH 120
DB 1 FDLVLRKESPKNIFFSPVSISSALMSLGAKGATQILEVLGNLTSETADH 60
QY 121 TYKELDTVTAPQK--NLKSASRIVFEXKLRKSSFVAPLEKSYGTRPR-VLTGNPRDL 177
DB 61 GFQHLHLNRPDKLQKLTANALFVDKSLKLDLSDFLVDKLYGAEVQSDSFAEEA 120
QY 178 -QEINNWNWQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLBEE 236
DB 121 KKQINDWVKKTKQKIKDLSLDLDPDTRVLVNAIVFKGKWKTFDPDPENTREDFYVDET 180
QY 237 RTVVRPNWSDPKAVLYRGDLSCKIAQLPLTGSMSIIFFLPKVTQNTLIEESLTSE 256
DB 181 TTVKVPWMSQTGRTFRYGRDEELNCQVLELYKGNASMLILPDE--GGLETVERKALTPE 238
QY 297 FIHIDRELKTQVAVLTVPKLSYGEVTKSLQEMKLSLQSLF--DSPDFSKIT-GPKIKLT 354
DB 239 TLKKWTKSLTKRSVELVLPKFLKLEISYDLKDXLVEKLGITDLFSNKADLSGISEDKOLKVS 298
QY 355 QVEHRACFEWNEEDGAGTTSPG--LQPAHLTFPLDVLHNPFFVLRDTRDTGALLPICKI 412
DB 299 KVVHKAFLVNEEGTEAAATGVIIVRSLP-PPEFRANRPFLFLIRDNPFTGSLFWGKV 357
QY 413 LDP 415
DB 358 VNP 360

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RESULT 12
US-10-023-634-88
; Sequence 88, Application US/10023634
; Publication No. US20030236389A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Colman, Steven D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Ballinger, Robert A
; APPLICANT: Guo, Xiaojia
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Li, Li
; APPLICANT: Ellerman, Karen
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shomir R
; APPLICANT: Gangolli, Esha A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-221
; CURRENT APPLICATION NUMBER: US/10/023,634
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/256,025
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/265,163
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,929
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/274,864
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,688
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,880
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/286,409
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/309,246
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/315,600
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 360
; TYPE: FAT
; ORGANISM: Homo sapiens
US-10-023-634-88

Query Match      25.3%; Score 538.5; DB 15; Length 360;
Best Local Similarity 33.6%; Pred. No. 4.7e-41;
Matches 122; Conservative 88; Mismatches 140; Indels 13; Gaps 9;

QY 63 YDLVRRSSMPTNNVLLSPVATLSALSLGAEORTESIIRALYYDL--TSSPDHNG 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 FDLVRELAKESPDKNIFSPVISLALSLGAKGSTATQILEVLGFTNLTSETADH 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 TYKELLDTVTAPQK-NLKASRVFEKLRKIKSFVAPELXSYGTRPR-VLTGPNRLDL 177
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GFQHLHLNLPDKNLQKLTANALFVDSKLLDLSFLEDVKLYGAEVQSDPDAEEA 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 178 -QEINNWWQAQMKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLDFYLD 236

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Db 121 KQINDWVKKTKGKIADLLSDLPDTRLVNVAIFYKGWKTPFPDENTREDFYVD 180
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 237 RTVRVPMMSDPKAVIRVGLSDLSCKIAQLPLTGSMSIIFPLPKVTQNLTLIESLTSE 296
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 TTVKVPMMSTQGRTRYGRDEELNCQVLELPYKGNASMLIILPDE--GGLTETVSKATP 238
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 297 FIHIDIRELKTQVAVLTVPKLKSVEGEVTKSLQEMKIQSLF-DSPDFSKIT-GKPIKLT 354
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 TLKKWTKSLTKRSVELYLPKFKLEISYDLKDVLEKLGITDLFSNKADLSIGSEDKLVS 298
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 355 QVEHRAGFEMNEDGAGITTPSEG--LQPAHLTFPLDYHINQPFIFVLRTDGTGALLFGKI 412
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 KVVHKAFLVNEEGTEAAATGVIIVPRSLP-PPEFKANRPFLLIRDNPTGSIIFMGKV 357
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 413 LDP 415
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 358 VNP 360
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
US-10-263-828-84
; Sequence 84, Application US/10263828
; Publication No. US20030138905A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: mammary gland and methods for their use.
; FILE REFERENCE: 11000.1044Uicon
; CURRENT APPLICATION NUMBER: US/10/263,828
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 125
; TYPE: FAT
; ORGANISM: Bovine
US-10-263-828-84

Query Match      23.4%; Score 499; DB 14; Length 125;
Best Local Similarity 83.3%; Pred. No. 4.1e-38;
Matches 105; Conservative 3; Mismatches 16; Indels 2; Gaps 1;

QY 1 MQALVLLLCIGALLCHSSCONPASPSPERGSDPDSTGALVEEDPFFKVPVKNLAAVSN 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MQALVLLLTGALLGFRCONAQO--EAGSLTPESTGAPVEEDPFFKVPVKNLAAVSN 58
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 FGVDLYRVRSSMPTNNVLLSPVATLSALSLGAEORTESIIRALYYDLISSPDHNG 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 59 FGVDLYRVRSGESPTANVLLSPVATLSALSLGAEORTESIIRALYYDLISSPDHNG 118
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 TYKELL 126
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 TYKDLL 124
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-09-823-187-31
; Sequence 31, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderna, Steven X
; APPLICANT: Spytek, Kimberly

```

APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
CURRENT FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 31
LENGTH: 377
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-31

Query Match 21.5%; Score 458.5; DB 10; Length 377;
Best Local Similarity 28.8%; Pred. No. 1.3e-33; Indels 25; Gaps 10;
Matches 113; Conservative 102; Mismatches 152

QY 34 DSTGALVEEDPFFKVPVVKLAARVNFYGVYRVRSSMPTTNVLLSPLSVATLSALS 93
DB 1 DSSRAL-----KLASANADFAFSLYKELVEQNPDKNIFSPVSISSALMLS 47

QY 94 LGAEQRTESIIRALYYDL--ISSPDHGTGYKELLDTVTAPQKNLK--SASRIVFEKLR 149
DB 48 LGAGNTATQILEVLGNLTETSEABHQFQHLQELNRPDTGLQLTGNALFVDSK 107

QY 150 IKSSFVAPLEKSYGTRP-RVLTGNPRDLQELNNWQAKMGKGLARSTKEIPDEISILL 208
DB 108 LLDEFLEDSKRLYQSEVFSVDFSDPEAKKQINDWVEKKTQGIKIDLLKDLSDTVLV 167

QY 209 GVAHFQGWTKDSRSTSLDYDEERTVRVPMMSDPKAVLRGLDSDLSCKTAQPL 268
DB 168 NYTFYFGKWKPPDPELTDEEDFHVDDKTVKVPMMNQ-LGTFYFPRDELNCKVLELP 226

QY 269 TG-SMSIIFPLPKVTONLTIBESLTSBFHIDRELKTVQAVLTVPKLSYGEVTK 327
DB 227 KGNATSMFLPDEVCK-LEQVEAALSPETKLNEMPREVELYLPKFSIECTYDLD 285

QY 328 SLOEMKLSLF-DSPFSKIT-GKPKLTQVHRAGFEWNEGAGTTPSPG--LOPAHLT 383
DB 286 VLAKLGITDLFSNQALSGISEDEDLKSVKAVKAVLEVDDEEGTAAAAATGAIIVPS 345

QY 384 FPDYHNLNPFIFVLRTDTGALLFGKILDP 415
DB 346 PILEFTADPPFLFIYDNTGSLFMCKVNP 377

RESULT 15

US-10-037-417-66
Sequence 66, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P

APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Store, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 66
LENGTH: 377
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Serpin
OTHER INFORMATION: Consensus Sequence
US-10-037-417-66

Query Match 21.3%; Score 453.5; DB 12; Length 377;
Best Local Similarity 28.6%; Pred. No. 3.9e-33;
Matches 112; Conservative 102; Mismatches 153; Indels 25; Gaps 10;

QY 34 DSTGALVEEDPFFKVPVVKLAARVNFYGVYRVRSSMPTTNVLLSPLSVATLSALS 93
DB 1 DSSRAL-----KLASANADFAFSLYKELVEQNPDKNIFSPVSISSALMLS 47

QY 94 LGAEQRTESIIRALYYDL--ISSPDHGTGYKELLDTVTAPQKNLK--SASRIVFEKLR 149
DB 48 LGAGNTATQILEVLGNLTETSEABHQFQHLQELNRPDTGLQLTGNALFVDSK 107

QY 150 IKSSFVAPLEKSYGTRP-RVLTGNPRDLQELNNWQAKMGKGLARSTKEIPDEISILL 208
DB 108 LLDEFLEDSKRLYQSEVFSVDFSDPEAKKQINDWVEKKTQGIKIDLLKDLSDTVLV 167

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2004, 11:09:24 ; Search time 40 Seconds
(without alignments)
1005.201 Million cell updates/sec

Title: US-10-619-149-1

Perfect score: 2131
Sequence: 1 MQALVLLICIGALLGHSSCO.....RDTDTGALLFIKILDPRGP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 781*

1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2125	99.7	418	2 A47281	pigment epithelial
2	1827	85.7	359	2 A46046	serine proteinase
3	470	22.1	432	2 S43977	alpha-2-antiplasmi
4	466.5	21.9	491	2 S47217	alpha-2-antiplasmi
5	456.5	21.4	491	1 ITHUA2	contrapsin precurs
6	455	21.4	410	2 C39088	alpha-1-antitryps
7	448	21.0	405	2 A39088	serine proteinase
8	443	20.8	403	2 S08102	serine proteinase
9	430.5	20.2	416	2 B29131	kalikrein-binding
10	427	20.0	418	1 ITHU	alpha-1-antitryps
11	421.5	19.8	388	2 B39088	alpha-1-antitryps
12	420	19.7	418	2 JX0129	contrapsin precurs
13	419.5	19.7	418	1 S31507	serine proteinase
14	418	19.6	409	1 ITBA	alpha-1-antitryps
15	418	19.6	418	2 S23675	contrapsin-related
16	417	19.6	406	2 JX0346	alpha-1-antitryps
17	416.5	19.5	418	2 JH0494	alpha-1-antitryps
18	415.5	19.5	406	2 I53281	corticosteroid-bin
19	414	19.4	411	1 ITRT	serine proteinase
20	413	19.4	412	2 S31505	serine proteinase
21	408	19.1	413	2 JX0154	alpha-1-antitryps
22	405.5	19.0	413	2 I49474	alpha-1-antitryps
23	404	19.0	379	2 A42421	leukocyte elastase
24	403.5	18.9	408	2 S11320	serine proteinase
25	403	18.9	413	2 JX0267	alpha-1-antitryps
26	403	18.9	416	2 S21097	alpha-1-antitryps
27	403	18.9	417	2 S19724	kalikrein-binding
28	396	18.6	413	2 S54981	alpha-1-antitryps
29	395.5	18.6	413	2 I56481	alpha-1-antitryps

30 395.5 18.6 500 1 ITHUC1 complement C1 inh
31 395 18.5 405 2 A28321 corticosteroid-bin
32 386 18.1 416 1 ITRSH alpha-1-antitryps
33 384 18.0 413 2 A54968 alpha-1-antitryps
34 382 17.9 418 2 A39567 thyroxine-binding
35 381.5 17.9 410 2 A45457 alpha-1-antitryps
36 381.5 17.9 427 2 A49518 kallistatin precu
37 380.5 17.9 413 2 I49470 alpha-1-antitryps
38 380.5 17.9 413 2 I49452 alpha-1-antitryps
39 379 17.8 383 2 A36117 corticosteroid-bin
40 378.5 17.8 413 2 I49472 alpha-1-antitryps
41 378.5 17.8 413 2 S60036 alpha-1-antitryps
42 377.5 17.7 402 2 I49471 alpha-1-antitryps
43 377.5 17.7 433 1 ITHUC alpha-1-antitryps
44 377 17.7 430 2 A49190 corticosteroid-bin
45 375.5 17.6 413 2 I49473 alpha-1-antitryps

ALIGNMENTS

RESULT 1

A47281 pigment epithelial-differentiating factor precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
R:Accession: A47281; S27967
R:Steele, F.R.; Chader, G.J.; Johnson, L.V.; Tombran-Tink, J.
Proc. Natl. Acad. Sci. U.S.A. 90, 1526-1530, 1993
A:Title: Pigment epithelium-derived factor: neurotrophic activity and identification as
submitted to the EMBL Data Library September 1991
A:Reference number: A47281; MUID:93165728; PMID:8434014
A:Accession: A47281
A>Status: Preliminary
A:Molecule type: DNA; protein
A:Residues: 1-418 <STEL>
A:Cross-references: GB:M76979; NID:G189777; PID:AAA60058.1; PID:G189778
A:Notes: Sequence extracted from NCBI backbone (NCBIN:124952, NCBI:P124953)
R:Steele, F.R.; Chader, G.J.; Johnson, L.V.; Tombran-Tink, J.
Submitted to the EMBL Data Library September 1991
A:Description: Pigment epithelium-differentiating factor (PEDF): Neurotrophic activity
ng.
A:Reference number: S27967
A:Accession: S27967
A:Molecule type: mRNA
A:Residues: 1-147,'X', 149-418 <STE2>
A:Cross-references: EMBL:M76979; NID:G189777
C:Genetics:
A:Gene: GDB:PEDF
A:Cross-references: GDB:138470; OMIM:172860
A:Map position: 17p13-17p13
C:Superfamily: Serpin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-418/Product: pigment epithelial-differentiating factor #status predicted <MAT>

Query Match 99.7%; Score 2125; DB 2; Length 418;
Best Local Similarity 99.5%; Pred. No. 1.6e-149;
Matches 416; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALVLLICIGALLGHSSCOQPASPPERSPPDPSTGALVEEDPFKVPYVKLAAYSN 60
Db 1 MQALVLLICIGALLGHSSCOQPASPPERSPPDPSTGALVEEDPFKVPYVKLAAYSN 60
QY 61 FGYDLYVRSSMPTTNVLLSPLSVATLSALSGAERTESIIRALYDYLISPDING 120
Db 61 FGYDLYVRSSMPTTNVLLSPLSVATLSALSGAERTESIIRALYDYLISPDING 120
QY 121 TYKEILLDTVTAPOKNLKSASRIVFEKKLRKSSFVAPLEKSYGTPRVLTGNPLDLOEI 180
Db 121 TYKEILLDTVTAPOKNLKSASRIVFEKKLRKSSFVAPLEKSYGTPRVLTGNPLDLOEI 180
QY 181 NNWVQAMQMKGLARSTKEIPDEISILLGLGVAHFQGWTKFDSRKTSLDEDFYLDERTVR 240
Db 181 NNWVQAMQMKGLARSTKEIPDEISILLGLGVAHFQGWTKFDSRKTSLDEDFYLDERTVR 240

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QY 241 VPMWDPKAVLRVGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIHD 300
Db 241 VPMWDPKAVLRVGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIHD 300
QY 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTSPGLQPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILDPRGP 418
Db 361 GFENWEDGAGTTSPGLQPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILDPRGP 418

RESULT 2
A46046
serine proteinase inhibitor homolog EPC-1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C;Accession: A46046
R;Pignolo, R.J.; Cristofalo, V.J.; Rotenberg, M.O.
J. Biol. Chem. 268, 8945-8957, 1993
A;Title: Senescent WI-38 cells fail to express EPC-1, a gene induced in young cells upon
A;Reference number: A46046; MUID:93232057; PMID:8473338
A;Accession: A46046
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-359 <PIG>
A;Experimental source: fetal lung-derived, fibroblast-like cells
A;Note: sequence extracted from NCBI backbone (NCBIP:129819)
C;Superfamily: Serpin

Query Match 85.7%; Score 1827; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.4e-127;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 NFGYDLVRVSSPTTNVLLSPVATLSALSGAEQRTESIHRALYDILSSPDH 119
Db 1 NFGYDLVRVSSPTTNVLLSPVATLSALSGAEQRTESIHRALYDILSSPDH 60
QY 120 GTYKELDTVAPQKNLKSASRVFVEKLRKSSFVAPLESYGTGPRVLTGNPLDQ 179
Db 61 GTYKELDTVAPQKNLKSASRVFVEKLRKSSFVAPLESYGTGPRVLTGNPLDQ 120
QY 180 INNVOAQMGKLRSTKEIPDEISILLGVAFKQWTKFDSKTSLEDFVLDERTV 239
Db 121 INNVOAQMGKLRSTKEIPDEISILLGVAFKQWTKFDSKTSLEDFVLDERTV 180
QY 240 RVPWSDPKAVLRVGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIH 299
Db 181 RVPWSDPKAVLRVGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIH 240
QY 300 DIDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEH 359
Db 241 DIDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEH 300
QY 360 AGFENWEDGAGTTSPGLQPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILDPRGP 418
Db 301 AGFENWEDGAGTTSPGLQPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILDPRGP 359

RESULT 3
S43977
alpha-2-antiplasmin precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1994 #sequence_revision 19-May-1995 #text_change 15-Sep-2003
C;Accession: S43977; S27260
R;Christensen, S.; Berglund, L.; Sottrup-Jensen, L.
FEBS Lett. 343, 223-228, 1994
A;Title: Primary structure of bovine alpha-2-antiplasmin.
A;Reference number: S43977; MUID:94229242; PMID:7513654
A;Accession: S43977
A;Molecule type: mRNA

QY 241 VPMWDPKAVLRVGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIHD 300
Db 241 VPMWDPKAVLRVGLDSDLSCKIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIHD 300
QY 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVQAVLTVPKLSYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEHRA 360
QY 361 GFENWEDGAGTTSPGLQPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILDPRGP 418
Db 361 GFENWEDGAGTTSPGLQPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILDPRGP 418

RESULT 4
S47217
alpha-2-antiplasmin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Sep-2003
C;Accession: S47217; S48204
R;Menoud, P.A.; Sappino, N.; Boudal-Khosbeian, M.; Vassalli, J.D.; Sappino, A.P.
submitted to the EMBL Data Library, August 1994
A;Description: The murine kidney is a major source of alpha 2-antiplasmin production.
A;Reference number: S47217
A;Accession: S47217
A;Molecule type: mRNA
A;Residues: 1-491 <MEN>
A;Cross-references: EMBL:Z36774; NID:G534037; PID:G534038
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48204
A;Molecule type: protein
A;Residues: 28-33 <LIJ>
C;Superfamily: Serpin

Query Match 22.1%; Score 470; DB 2; Length 492;
Best Local Similarity 30.2%; Pred. No. 6.2e-27;
Matches 120; Conservative 75; Mismatches 175; Indels 28; Gaps 7;

QY 22 PASPPPEEG--SPDPDSTGALVEEEDPPFKVFNKLAASVNFYDLYRVSSMSPTTNVL 79
Db 64 PKKAPEDCKLSPTPEQT-----RLAFAMMTFTTDLPSLVAQSSTRPNLI 108
QY 80 LSPUSVATLSALSGAEQRTESIHRALYDILSSPDHGTYKELDTVAPQKNLKS 139
Db 109 LSPUSVATLSALSGAEQRTESIHRALYDILSSPDHGTYKELDTVAPQKNLKS 164
QY 140 SRIVFEKLRKSSFVAPLESYGTGPRVLTGNPLDQINNVOAQMGKLRSTKEI 199
Db 165 ARMYLQKGPFIKEDFLQSQSLFGAKPMSLTGKMGEDLANINWVREATGKIEDFLSDL 224
QY 200 PDETSILLGVAFKQWTKFDSKTSLEDFVLDERTVVRPMMSDPPKAVLRVGLDSDL 259
Db 225 PDDTVLLLNALHFQGFWRSKFDPNLTQFGAFHLDQFTVFVDMQALTYPLHFWLLEQP 284
QY 260 SCTIAQLPLTGSMISIIFFLPKVTQNTLTIEESLTSEFIHDIDRELKTVQAVLTVPK 319
Db 285 EIQVAFHPPKNNMSFVLMPTREFWASQVLANLTWDLH--QPSLSERTKYQLPKLHL 342
QY 320 SYEGEVTKSLQEMKLSQSFSPSKITGPKIKLTQVEHRAGFENWEDG--AGTTSPGL 377
Db 343 KYQLDVLATLSQLGLQELFQAPDLRGISDERLVSVSVQHSQALELSEAGVQAAAAATSTAM 402
QY 378 QPAHLTFPDLVHLNQPFIFVLRTDTGALLFGIKILD 415
Db 403 SRMSLS---SFIVNRPFLFFILEDSTSLPLFVGSVRNP 437
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Query Match 21.9%; Score 466.5; DB 2; Length 491;
Best Local Similarity 31.7%; Pred. No. 1.1e-26;
Matches 116; Conservative 75; Mismatches 162; Indels 13; Gaps 5;

QY 53 KLAARVNFYGYDLVRSSMSPTTNVLLSPISVATALSALSLGAEQRTSGIIHRLAYDL 112
DB 81 RLQAQMAFTTDLFSLVAQTSTSNVLSPISVALSHLAGAQNCTLSLHRVLMNT 140
QY 113 ISS-PDIHGTYKELLDTVAPQKNLKSASRIIVFKKURIKSSFVAPLEKSYGTRPRVLVT 171
DB 141 GSCPLPHLSHFYQNLGPGT-----IRLAARIYLOKGFPIKDDELEQSEQRFLGAKPVKLTV 195
QY 172 NPLDLOEINNVOAQMKLARGTKEIPDEISILLGVAFKGOVTKEDSKTSLEDF 231
DB 196 KOEDLANINQWKEATEGKIEDFLSELPDSTVLLLNALHFGFWTKEDPSLTQKDF 255
QY 232 YLDEBTRVPMSPDKAVIRYGDSDLSCSKIAQLPTGSMISIFFPLPKVTQNLTLIEE 291
DB 256 HLDERTVSDMHAIVSPLRFLEQPEIQVAHFPPKNNMSFVVVMTYFENNVSEVLA 315
QY 292 SLTSEFIHDIDRELKTVQAVLTVPEKLSVEGEVTKSLQEKLSLPDSDPSKITCKPI 351
DB 316 NLTWDTYHPSLQSRPTKVMW--PKHLQOQLDLVATLSQLGQELFQGPLRGISEQNL 373
QY 352 KLTQVHRAGFEMNEDG--AGTTSPGLQPAHLTFPLDYHLNPPFFIVFLRDTDTGALLFI 409
DB 374 WVSSVQHQSTWELSEAGVERAAATSVAMNMSLS---SFTVNRPLFFIMEDTIGVPLFV 430
QY 410 GKILDP 415
DB 431 GSVNRP 436

RESULT 5
ITHUA2
alpha-2-antiplasmin precursor [validated] - human
N/Alternate names: alpha-2-FI; alpha-2-plasmin inhibitor precursor
C/Species: Homo sapiens (man)
C/Date: 31-Jul-1989 #sequence revision 12-Apr-1996 #text change 15-Sep-2003
C/Accession: A31402; A32163; A41504; A26684; A24708; PC2129; S00068; S32524; S32529
R/Hiroawa, S.; Nakamura, Y.; Miura, O.; Sumi, Y.; Aoki, N.
Proc. Natl. Acad. Sci. U.S.A. 85, 6846-6849, 1988
A/Title: Organization of the human alpha-2-plasmin inhibitor gene.
A/Reference number: A31402; MUID:88320531; PMID:3166140
A/Accession: A31402
A/Molecule type: DNA
A/Residues: 1-491 <HIR1>
A/Cross-references: GB:M20786; GB:J03830; NID:g177884; PIDN:AAAS1554.1; PID:g177886
R/Hiroawa, S.; Nakamura, Y.; Miura, O.; Sumi, Y.; Aoki, N.
Proc. Natl. Acad. Sci. U.S.A. 86, 1612-1613, 1989
A/Reference number: A32163
A/Accession: A32163
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-491 <HIR2>
R/Tone, M.; Kikuno, R.; Kume-Iwaki, A.; Hashimoto-Gotoh, T.
J. Biochem. 102, 1033-1041, 1987
A/Title: Structure of human alpha-2-plasmin inhibitor deduced from the cDNA sequence.
A/Reference number: A41504; MUID:88139254; PMID:2830248
A/Accession: A41504
A/Molecule type: mRNA
A/Residues: 1-32, 'W', 34-491 <TON>
A/Cross-references: GB:D00174; NID:g219409; PIDN:BAA00124.1; PID:g219410
R/Holmes, W.E.; Nelles, L.; Liijnen, H.R.; Collen, D.
J. Biol. Chem. 262, 1659-1664, 1987
A/Title: Primary structure of human alpha-2-antiplasmin, a serine protease inhibitor (se
A/Reference number: A26684; MUID:87109313; PMID:2433286
A/Accession: A26684
A/Molecule type: mRNA
A/Residues: 4-286, 'D', 290-491 <HOL>
A/Cross-references: GB:J02654; NID:g178750; PIDN:AAA35543.1; PID:g178751
A/Note: the authors translated the codon GAT for residue 289 as His
R/Sumi, Y.; Nakamura, Y.; Aoki, N.; Sakai, M.; Muramatsu, M.

J. Biochem. 100, 1399-1402, 1986
A/Title: Structure of the carboxyl-terminal half of human alpha-2-plasmin inhibitor ded
A/Reference number: A24708; MUID:87137400; PMID:3818581
A/Accession: A24708
A/Molecule type: mRNA
A/Residues: 218-491 <SUM>
A/Cross-references: DDBJ:D00116; NID:g219407; PIDN:BAA00070.1; PID:g219408
R/Koyama, T.; Koike, Y.; Toyota, S.; Miyagi, F.; Suzuki, N.; Aoki, N.
Biochem. Biophys. Res. Commun. 200, 417-422, 1994
A/Title: Different NH2-terminal form with 12 additional residues of alpha2-plasmin inhi
A/Reference number: PC2129; MUID:94220119; PMID:8166714
A/Accession: PC2129
A/Molecule type: protein
A/Residues: 28-53 <KOY>
A/Experimental source: Hep G2 cells cultured in serum-free medium
A/Note: In the presence of serum, this material loses the first twelve residues and bec
R/Liijnen, H.R.; Holmes, W.E.; Van Hoef, B.; Wiman, B.; Rodriguez, H.; Collen, D.
Eur. J. Biochem. 166, 565-574, 1987
A/Title: Amino-acid sequence of human alpha-2-antiplasmin.
A/Reference number: S00068; MUID:87275946; PMID:2440681
A/Accession: S00068
A/Molecule type: protein
A/Residues: 40-48, 'G', 50-104, 'D', 106-114, 'X', 116-327, 'X', 329-340, 'XXX', 345-407, 'G', 409
A/Note: 49-Gly and 408-Gly may represent heterogeneity; 2 disulfide bonds were determin
R/Bangert, K.; Johnsen, A.H.; Christensen, U.; Thorsen, S.
Biochem. J. 291, 623-625, 1993
A/Title: Different N-terminal forms of alpha(2)-plasmin inhibitor in human plasma.
A/Reference number: S32524; MUID:93249387; PMID:8484741
A/Accession: S32524
A/Molecule type: protein
A/Residues: 28-58 <BAN>
R/Engbild, J.J.; Valnickova, Z.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
Biochem. J. 291, 933-938, 1993
A/Title: An examination of the inhibitory mechanism of serpins by analysing the interac
A/Reference number: S32529; MUID:93256910; PMID:7693878
A/Accession: S32529
A/Molecule type: protein
A/Residues: 28-43; 64-69; 405-409 <ENG>
A/Note: determination of cleavage and inhibitory sites
R/Sumi, Y.; Ichikawa, Y.; Nakamura, Y.; Miura, O.; Aoki, N.
J. Biochem. 106, 703-707, 1989
A/Title: Expression and characterization of Pro alpha-2-plasmin inhibitor.
A/Reference number: A57869; MUID:90110073; PMID:2606916
A/Contents: annotation; role of propeptide
R/Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986
A/Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A/Reference number: A32585; MUID:87057190; PMID:2877981
A/Contents: annotation; cross-linking site for fibrin
C/Comment: After synthesis in the liver, 30-50% of alpha-2-antiplasmin circulates in pl
inhibit activated coagulation factor XIII from forming an isopeptide cross-link with f
C/Genetics:
A/Gene: GDB:PLI
A/Cross-references: GDB:120301; OMIM:262850
A/Map position: 17pter-17p12
A/Introns: 21/3; 34/3; 55/3; 123/1; 171/1; 239/1; 286/3; 355/1
C/Functions:
C/Description: moderates fibrinolysis by inhibiting plasmin
C/Superfamily: Serpin
C/Keywords: extracellular protein; fibrinolysis; glycoprotein; plasma; serine proteinas
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-39/Domain: propeptide #status experimental <PRO>
F:40-491/Product: alpha-2-antiplasmin #status experimental <MAT>
F:454-465/Domain: amphipathic helix #status predicted <APH>
F:465-467/Region: cell attachment (R-G-D) motif
F:39-40/Cleavage site: Pro-Asn (unidentified plasma proteinase) #status experimental
F:41/Cross-link: isopeptide (Gln) (interchain to Lys-322 of fibrin alpha chain) #status
F:70-152, 103-143/Disulfide bonds: #status experimental
F:126, 295, 309, 316/Binding site: carboxylate (Asn) (covalent) #status experimental
F:403-404/Cleavage site: Arg-Met (chymotrypsin) (partial) #status experimental
F:403/Inhibitory site: Arg (plasmin) #status predicted
F:404-405/Cleavage site: Met-Ser (chymotrypsin) (partial) #status experimental

F;404/Inhibitory site: Met (chymotrypsin) #status predicted
F;437/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 21.4%; Score 456.5; DB 1; Length 491;
Best Local Similarity 28.4%; Pred. No. 6.2e-26;
Matches 127; Conservative 86; Mismatches 181; Indels 53; Gaps 11;

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QY 5 VLLICIGALLGHSCQNPAS-----PPEE-----GSPDPDSTGAL--- 39
DB 7 LLVLSWCLQGPCVSVFVSGAMPGLGRLTSGNQSVSPLTLKLGNEPFGQGTALKSP 66
QY 40 --VEEEDFFKVP--VNKLAAAVSNFGYDIYRVSSMSPTTNVLLSPLSVATALSALSG 95
DB 67 PGVCSRDp---TPEQTHRLARAMMAFTADLFSVAQSTCTCPNLILSPLSVATALSALG 123
QY 96 AE-----ORTESIHRALYDILSSPDHGTGTYKELLDTVTAPOKNLKSASRIVPEKLR 151
DB 124 AQNHTLQRLQOVLAG-----SGPCLPHLLSLRCODLPGAPRL--AARMYLQKGFPIK 175
QY 152 SSFVAPLEKSGYTRPRVLTGNPRLDLOEINNVAQWQMGKLARSTKEIPDEISILLGVA 211
DB 176 EDFLEQSEQLFGAKPVSLTGQEDDLANINQWKEATGKIQFSLGSLPEDTVLLLLNAI 235
QY 212 HFQGWTKFDSRKTSLIEDYLBERTVRVPMMSDPKAVLYRGDLSLCKIAQLPLTGS 271
DB 236 HFQGFWRNKFDPSTLQDSFHLDEQFTVPVVMNQARTYPLRWFLLEQPEIQVAHFPPKN 295
QY 272 MSIIFFPLKVTQNLTLIESLTSEFTHD--IDRELKTQVAVLTVPKLSVEGEVTKS 328
DB 296 MSFVLVPTHEWVSQVLANLWDTLHPPLVVERPTK-----VRLPKLYLKHQMDLVAT 350
QY 329 LQEMKLSQSFDSFDSKITQPKIKLTQVEHRAQFEMNEDGAGTTPSPGLQPAHLTPLDY 388
DB 351 LSQGLQELCAPDLRGISQSLVSGVQHS*LELSEGVAAATSIAMSRMSLS-SF 409
QY 389 HLNQPPFVLRDITDGTGALLFGKILDP 415
DB 410 SVNRPFLLFFIEDTGLPLFVGKVMDP 436

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RESULT 6

C39088

contrapsin precursor - guinea pig

C:Species: Cavia porcellus (Guinea pig)

C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 15-Sep-2003

C:Accession: C39088

R;Suzuki, Y.; Yoshida, K.; Honda, E.; Sinohara, H.

J. Biol. Chem. 266, 928-932, 1991

A:Title: Molecular cloning and sequence analysis of cDNAs coding for guinea pig alpha-1-

A:Reference number: A39088; MUID:91093294; PMID:1985973

A:Accession: C39088

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-410 <SUZ>

A:Cross-references: GB:M38573

C:Superfamily: Serpin

Query Match 21.4%; Score 455; DB 2; Length 410;

Best Local Similarity 28.1%; Pred. No. 6e-26;

Matches 111; Conservative 101; Mismatches 159; Indels 24; Gaps 9;

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QY 37 GALVEE---EDPPFKVPVNVKLAASVNFYDIYRVSSMSPTTNVLLSPLSVATALSAL 92
DB 21 GIMAEITQVAQVPSQHPKSVPRSLAHFAHSMYRVLTQGSNTSNIFFSVSTATALAW 80
QY 93 SLGAQRTESIHRALYDIL--ISSPDHGTGTYKELLDTVTAPOKNLKSASRIVPEK 148
DB 81 SLGAGDGTHTQILKSLSEFNLTAEADIDHGFQNLHLTLNRPHSEHQLTTGNGLFDQNL 140
QY 149 RIKSSFVAPLEKSGYTRPRVLTGNPRLDLOEINNVAQWQMGKLARSTKEIPDEISILL 207
DB 141 KLEKFGSDVKTLYHAEAFPTNFSNPKAEKQINAVYVEKGTQGIKIVDLVYKDLGADIVLAL 200

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QY 208 LGVAHFQGWTKFDSRKTSLIEDYLBERTVRVPMMSDPKAVLYRGDLSLCKIAQ-- 265
DB 201 VNYIFFRGKWEKPFVDVXHTTQEDFHVDAANTVTKVPMK-----QQGMHKAFCSTIQSW 254
QY 266 ---LPLTGSMSIIFPLPKVTQNLTLIESLTSEFTHDRELKTQVAVLTVPKLSVE 322
DB 255 VLLLDYEGNVTAFLPDE--GKMQHLEETLTPELVFKFLRKTETMPAYVSLPKLSISGT 312
QY 323 GEVTKSLQEMKLSQSFDSKIT--GKPIKLTQVEHRAQFEMNEDGAGTTPSPGLQPA 380
DB 313 YDLKEVLRDITDGTGALLFGKILDP 415
QY 381 HLTPLDYHLNQPPFVLRDITDGTGALLFGKILDP 415
DB 373 RTARPPRLSPNKPFFFLIIDHSTDTPLFVGKVMDP 407

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RESULT 7

A39088

alpha-1-antiprotease S precursor - guinea pig

C:Species: Cavia porcellus (Guinea pig)

C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 15-Sep-2003

C:Accession: A39088

R;Suzuki, Y.; Yoshida, K.; Honda, E.; Sinohara, H.

J. Biol. Chem. 266, 928-932, 1991

A:Title: Molecular cloning and sequence analysis of cDNAs coding for guinea pig alpha-1-

A:Reference number: A39088; MUID:91093294; PMID:1985973

A:Accession: A39088

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-405 <SUZ>

A:Cross-references: GB:M38571

C:Superfamily: Serpin

Query Match 21.0%; Score 448; DB 2; Length 405;

Best Local Similarity 28.3%; Pred. No. 2e-25;

Matches 110; Conservative 98; Mismatches 161; Indels 20; Gaps 8;

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QY 39 LVEEDPFFKVPVNVKLAASVNFYDIYRVSSMSPTTNVLLSPLSVATALSALSGAEQ 98
DB 22 IMAEDAQVAQFSQQIPRSLAHFAHSMYRVLTQGSNTSNIFFSVSTATALAMVSVGAKG 81
QY 99 RTESIHRALYDIL--ISSPDHGTGTYKELLDTVTAPOKNLKSASRIVPEKLRKSS 154
DB 82 DTHQILRGLEFNLTAEADIDHGFQNLHLTLNRPHSEHQLTTGNGLFDQKLKKEF 141
QY 155 VAPLEKSGYTRPRVLTGNPRLDLOEINNVAQWQMGKLARSTKEIPDEISILLGVAHF 213
DB 142 SEDVKTLYHAEAFPTNFSNPKAEKQINAVYVEKGTQGIKIVDLVYKDLGADIVLAVNYIFF 201
QY 214 KGWVTKFDSRKTSLIEDYLBERTVRVPMMSDPKAVLYRGDLSLCKIAQ-----LPL 268
DB 202 RKNKEKPDVXHTTQEDFHVDTSTTVKPMK-----REGKYKAFHCSTIQSWILLDY 255
QY 269 TGSMSIIFPLPKVTQNLTLIESLTSEFTHDRELKTQVAVLTVPKLSVEGEVTKS 328
DB 256 EGNVTALFLLPEE--GKMQHLEETLTPELVFKFARKTERMFANVHLPKLSISGTIDYLV 313
QY 329 LQEMKLSQSFDSKITQK--PIKLTQVEHRAQFEMNEDGAGTTPSPGLQPAHLTFLP 386
DB 314 LGHLGITNVFSDAADLGSVTEIDPLKLSKGLHALLTIDKGTAAAGATWTFEFPNLSPE 373
QY 387 DYHLNQPPFVLRDITDGTGALLFGKILDP 415
DB 374 DLSFNKPFLLIIDHSTDTPLFVGKVMDP 402

```

RESULT 8

S08102

serine proteinase inhibitor 1 - rat

N:Alternate names: growth hormone-induced proteinase inhibitor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 15-Sep-2003

C;Accession: S08102; S11318; A29131
R;le Cam, A.
Submitted to the EMBL Data Library, August 1989
A;Reference number: S08099
A;Accession: S08102
A;Molecule type: mRNA
A;Residues: 1-403 <LEC>
A;Cross-references: EMBL:X16357; NID:G57230; PIDN:CAA34406.1; PID:G57231
R;Pages, G.; Rouayrenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
Eur. J. Biochem. 190, 385-391, 1990
A;Title: Molecular characterization of three rat liver serine-protease inhibitors affected by growth hormone
A;Reference number: S11318; MUID:90306038; PMID:1694763
A;Accession: S11318
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-403 <PAG>
A;Cross-references: EMBL:X16357; NID:G57230; PIDN:CAA34406.1; PID:G57231
R;Yoon, J.B.; Towle, H.C.; Seelig, S.
J. Biol. Chem. 262, 4284-4289, 1987
A;Title: Growth hormone induces two mRNA species of the serine protease inhibitor gene 4
A;Reference number: A92632; MUID:87166046; PMID:3494016
A;Accession: A29131
A;Molecule type: mRNA
A;Residues: 82-234, 'L', 236-403 <YOO>
A;Cross-references: GB:M15917; GB:J02692; NID:G207041; PIDN:AAA42172.1; PID:G207042
C;Superfamily: Serpin

Query Match 20.8%; Score 443; DB 2; Length 403;
Best Local Similarity 30.5%; Pred. No. 4.5e-25;
Matches 113; Conservative 82; Mismatches 166; Indels 10; Gaps 7;

QY 54 LAAAVSFGDLYRVRSSMPTTNVLLSPLSVATLSALSGAQRTEIIRHLYYDL- 112
DB 35 LASNTDFALSLYKLLALRNPDKNVFSPISIALTILSLGAKDSTMBEILGLKFNLT 94

QY 113 -ISSPDHGTIKELDTVTAP--QKNLKSASRIVFEKKRIKSFVAPLEKSYGTGPRVL 169
DB 95 EITEEIHQGFHLLQSQPEDQVEINTGSALPIDKEQPISEFQSKTRALYQAFIA 154

QY 170 T-GNPRDLQEIINNVAQMKGLARSTKIPDEISILLGVAFKQWTKYDSKTSLS 228
DB 155 DFKQPNRAKLLINDVSNQTKIAELFSLSERTSMVLVNYLLFKGKVKVPNPNDTFE 214

QY 229 EDFYLDERTVVRPMWSDPKAVLYGLDLSLCKIAQLPLTGMSSIIFFFLPKVTQNLTL 288
DB 215 SEFYLDKRSVKVPMWKEVTTTPYVRDELSLCSVLEKVTGNASALFILPDQ--GKMQ 272

QY 289 IEBSLTSEFTHD-IDRELKTVQAVLTPVKLKSVEGEVTKSLQBMKLSLF-DSPDPSKI 346
DB 273 VESSLOPETLKKKXDSLPIRIINDLRMPKFSISTDYSLSKEVLPGLGKIKVFSQADLSRI 332

QY 347 TG-KPIKLTQVEHRAGFEWEDGAGTTPSPQLQPAHLTFPLDYLHNLQPFIFVLRLDTGA 405
DB 333 TGTLDLYSQVHVKAIVDVBGTGEATATGATVIRQRPTLNFRFPFVVITDMSQS 392

QY 406 LLFVGKILDDR 416
DB 393 ILFVAKITNPK 403

RESULT 9
B29131
Kallikrein-binding protein precursor - rat
N;Alternate names: contraptin-like protease
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 sequence revision 31-Mar-1989 #text change 15-Sep-2003
C;Accession: B29131; A29448; S11319; JN0106; A40810; A37889; JX0156; S08039; S08101
R;Yoon, J.B.; Towle, H.C.; Seelig, S.
J. Biol. Chem. 262, 4284-4289, 1987
A;Title: Growth hormone induces two mRNA species of the serine protease inhibitor gene 4
A;Reference number: A92632; MUID:87166046; PMID:3494016
A;Accession: B29131
A;Molecule type: mRNA

A;Residues: 1-416 <YOO>
A;Cross-references: GB:M15916; GB:J02692; NID:G207043; PIDN:AAA42173.1; PID:G207044
R;le Cam, A.; Pages, G.; Auberger, P.; le Cam, G.; Leopold, P.; Benarous, R.; Glaichenh
EMBO J. 6, 1225-1232, 1987
A;Title: Study of a growth hormone-regulated protein secreted by rat hepatocytes: cDNA
A;Reference number: A29448; MUID:87275813; PMID:2440672
A;Accession: A29448
A;Molecule type: mRNA
A;Residues: 1-97, 'V', 99-416 <LEC>
R;Pages, G.; Rouayrenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
Eur. J. Biochem. 190, 385-391, 1990
A;Title: Molecular characterization of three rat liver serine-protease inhibitors affected by growth hormone
A;Reference number: S11318; MUID:90306038; PMID:1694763
A;Accession: S11319
A;Molecule type: mRNA
A;Residues: 11-97, 'V', 99-112, 'H', 113-386, 'P', 388-416 <PAG>
A;Cross-references: EMBL:X16358; NID:G57232; PIDN:CAA34407.1; PID:G57233
R;Pages, G.; Rouayrenc, J.F.; Rossi, V.; le Cam, G.; Mariller, M.; Szpirer, J.; Szpirer
Gene 94, 273-282, 1990
A;Title: Primary structure and assignment to chromosome 6 of three related rat genes en
A;Reference number: JN0106; MUID:91078650; PMID:2258058
A;Accession: JN0106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 11-97, 'V', 99-325, 'D', 327-416 <PA2>
A;Cross-references: GB:X16362; NID:G57236; PIDN:CAA34409.1; PID:G57237
A;Experimental source: liver
R;Chai, K.X.; Ma, J.X.; Murray, S.R.; Chao, J.; Chao, L.
J. Biol. Chem. 266, 16029-16036, 1991
A;Title: Molecular cloning and analysis of the rat kallikrein-binding protein gene.
A;Reference number: A40810; MUID:91340751; PMID:1874745
A;Accession: A40810
A;Molecule type: DNA
A;Residues: 1-55, 'L', 53-97, 'V', 99-416 <CHA>
A;Cross-references: GB:IM67496
A;Note: the authors translated the codon CTC for residue 52 as Phe
R;Chao, J.; Chai, K.X.; Chen, L.M.; Xiong, W.; Chao, S.; Woodley-Miller, C.; Wang, L.;
J. Biol. Chem. 265, 16394-16401, 1990
A;Title: Tissue kallikrein-binding protein is a serpin. Purification, characterization,
A;Reference number: A37889; MUID:90375506; PMID:2398056
A;Accession: A37889
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-49 <CH2>
R;Ohkubo, K.; Ogata, S.; Misumi, Y.; Takami, N.; Ikehara, Y.
J. Biochem. 109, 243-250, 1991
A;Title: Molecular cloning and characterization of rat contraptin-like protease inhibit
A;Reference number: JX0156; MUID:91324305; PMID:1864837
A;Accession: JX0156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-69, 'C', 71-72, 'A', 74-193, 'D', 195-249, 'V', 251-384, 'V', 386-416 <CHK>
C;Genetics:
A;Introns: 211/1; 302/2; 352/3
C;Superfamily: Serpin
C;Keywords: glycoprotein; serine proteinase inhibitor

Query Match 20.2%; Score 430.5; DB 2; Length 416;
Best Local Similarity 30.5%; Pred. No. 4e-24;
Matches 116; Conservative 80; Mismatches 157; Indels 27; Gaps 10;

QY 54 LAAAVSFGDLYRVRSSMPTTNVLLSPLSVATLSALSGAQRTEIIRHLYYDL- 112
DB 45 LASINTDFSLYKLLALRNPDKNVFSPISIALTILSLGAKDSTMBEILGLKFNLT 104

QY 113 -ISSPDHGTIKELDTVTAP--QKNLKSASRIVFEKKRIKSFVAPLEKSYGTGPRVL 169
DB 105 EITEEIHQGFHLLQSQPEDQVEINTGSALPIDKEQPISEFQSKTRALYQAFV- 163

QY 170 TGNPRDLQEI-NNVVAQMKGLARSTKIPDEISILLGVAFKQWTKYD 222
DB 164 ----ADPKQCNEAKKFINDVYSNQTQKIAELFSELQERTSMVLVNYLLFKGKVKVPFN 218

A;Residues: 196-225 <LE12>
A;Cross-references: GB:J00066; NID:g177819; PIDN:AAB59370.1; PID:g177823
R;Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem. J. 314, 647-653, 1996
A;Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A;Reference number: S63599; MUID:96239126; PMID:8670081
A;Accession: S63599
A;Molecule type: protein
A;Residues: 371-385 <CHA>
R;Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williams, R.
Biomed. Biochim. Acta 44, 421-431, 1985
A;Title: Construction and partial characterization of a human liver cDNA library.
A;Reference number: I39370; MUID:85225507; PMID:3873938
A;Accession: I39370
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 387-399, 'D', 401-418 <COU>
A;Cross-references: GB:M26123; NID:g177815; PIDN:AAAS1545.1; PID:g177816
R;Faber, J.P.; Weidinger, S.; Olek, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A;Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zugsburg.
A;Reference number: A35338; MUID:90252805; PMID:2339709
A;Accession: A35338
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 122-124, 'H', 126-128/363-365, 'K', 367-369 <FAB>
A;Experimental source: mutant PI Zugsberg
A;Note: this Z mutation with Lys-366 arose from the M2 variant with His-125
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50775; PDB:7AP1
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50794; PDB:8AP1
A;Contents: annotation; X-ray crystallography, 3.1 angstroms, hexagonal form, residues 4
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50810; PDB:9AP1
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 2, residue
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
J. Mol. Biol. 177, 531-556, 1984
A;Title: Human alpha-1-proteinase inhibitor. Crystal structure analysis of two crystal
A;Reference number: A58525; MUID:84292309; PMID:6332197
R;Carrell, R.W.; Jeppsson, J.O.; Vaughan, L.; Brennan, S.O.; Owen, M.C.; Boswell, D.R.
FEBS Lett. 135, 301-303, 1981
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Reference number: A58526; MUID:82095611; PMID:6976274
A;Contents: annotation; carbohydrate attachment sites
C;Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indiv
sis.
C;Genetics:
A;Gene: GDB:PI
A;Cross-references: GDB:120289; OMIM:107400
A;Map position: 14q32.1-14q32.1
A;Introns: 216/1; 306/2; 355/3
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: inhibitor of serine proteinases, primarily leukocyte elastase and collagen
A;Note: it also inhibits plasmin, thrombin, kallikrein, trypsin, and chymotrypsin
C;Superfamily: Serpin
C;Keywords: acute phase; emphysema; glycoprotein; plasma; polymorphism; serine proteinase
F.1-24/Domain: signal sequence #status predicted <SIG>
F.25-418/Product: alpha-1-antitrypsin #status experimental <MAT>
F.70.107.271/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.382/Inhibitory site: Met (elastase, collagenase) #status experimental
Query Match 20.0%; Score 427; DB 1; Length 418;
Best Local Similarity 28.2%; Pred. No. 7.3e-24; Indels 42; Gaps 13;
Matches 120; Conservative 93; Mismatches 170;
13 LLGHSSCONPASPPEGSFDPDSTGALV-----EEEDFFKVPVKNLAAAVSNFGYDLY 66

QY

Db 11 LLAGLCCLVPVSLAE-----DPOGDAAQXTDTSHPDQDHTP-----NKITPNLAEAFASLY 62
QY 67 VRRSMSPTTNVLLSPLSVATLSALSQAERTESIHRALYDLSPPD---HGTYKE 124
Db 63 RQLAHQSNTNIFPSVSIATAFAMLSLGTADTDEILEGNFNLTIPEAQIHGFGQE 122
QY 125 LLDTVTAP--QKNLSASRIVFEKLRISKSVPAPLESYGRTP-RVLTGNPRLDLQELN 181
Db 123 LLRTLNQPSOQLTGTNGFLFSEGLKLVDFELEDVKLYHSEATVNFQDTEAAKQIN 182
QY 182 NVVQAMQMGKLAARSTKEIPDEISILLGVAFHKGQVTKSPKRTSLDSDFYLDERTVRV 241
Db 183 DYVEKGTQGIKVDLVKELDRDTVFALVNYIFFKGWERPFVFKDTEEDFHDVQVTVKV 242
QY 242 PMSDPKAVLRVYGLSDLSCK-----IAQLPLTGSMSIIFPLPLKVTQNLTLIEESLT-- 294
Db 243 PMWK-----RUGMFINIQCKKLSWLLMKYLNATAIFFLPDE--GKLQHLENELTHD 294
QY 295 --SETHIDIRELKTQVAVLTVPKLSYEGSVTKSLOEMKLSLF--DSPDFSKITGK-P 350
Db 295 IITKPLENEDRR---SASLHLPKLSITGTYDLKSVLGQGITKVFSGADLSGVTEAP 350
QY 351 IKLTQVHRPAGFENWEDGAGTTFSGLOPAHITFPDLYHLNQPFIVLRTDITGALLFIG 410
Db 351 LKLSKAVHKAVLTIDEKGTAAAGAMFLEAIPMSIPEVKFNAPFVFLMIEQTKSPFMG 410
QY 411 KILDP 415
Db 411 KVNP 415
RESULT 11
B39088
alpha-1-antitrypsin F precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 15-Sep-2003
C;Accession: B39088
R;Suzuki, Y.; Yoshida, K.; Honda, E.; Sinohara, H.
J. Biol. Chem. 266, 928-932, 1991
A;Title: Molecular cloning and sequence analysis of cDNAs coding for guinea pig alpha-1
A;Reference number: A39088; MUID:91093294; PMID:1985973
A;Accession: B39088
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-388 <SUZ>
A;Cross-references: GB:M38572
C;Superfamily: Serpin
Query Match 19.8%; Score 421.5; DB 2; Length 388;
Best Local Similarity 28.5%; Pred. No. 1.7e-23;
Matches 111; Conservative 88; Mismatches 155; Indels 35; Gaps 10;
QY 39 LVEEEDFPFKVPVKNLAAAVSNFGYDLYRVRSMSPPTTNVLLSPLSVATLSALSLSGASQ 98
Db 20 IMAEDAQAQVAGPSQQ:PRSLAHFAHMYRVLTCQSNSTNIFPSVSIATLAAVMSLGAKG 79
QY 99 RIESIHRALYDLYL--ISSPDINGTYKELLDTVTAP--QKNLSASRIVFEKLRITKSSP 154
Db 80 DTHQTILWGLEFNLTIEADIDHGQNLNLTNRPHSEHETGTGFLFDQNLKUKERF 139
QY 155 VAPLESYGRTPRVLT-GNPRDLQELNNVQAQMGKLAARSTKEIPDEISILLGVAFH 213
Db 140 SEDVKTYLHAEAPPTNFSNPKAEKQINAYVEKGTQGIKVDLVKLSADTLVALVNYIFF 199
QY 214 KGQVTKFSKRTSLDEDFYLDERTVRVPMMSDPKAVLRVYGLSDLSCKIAQ-----LPL 268
Db 200 RKGWEKPFVYKHTTQEDFLVDMNTTNNVPMK-----RQGMKAFHCSTIOSWLLDY 253
QY 269 TGSMSIIFPLKVTQNLTLIEESLSEFIHIDIRELKTQVAVLTVPKLSYEGSVTKS 328
Db 254 EGNVTILFLPDK--GKMQHLEETLTPELIFKARKTERMFANVHLPKLSISGTYDLKEV 311

QY 329 LQEMKLOSLFD-SPDFSKIT-GKPIKLTQVEHRAFGFENNEDGAGTTPSPGQPAHLTFPL 386
 Db 312 LHLGITNVFGADLSGITDELKIR-----BAAGATE---LEITPHSVPO 356
 QY 387 DYHLNQPFIVLRDPTDGTGALLFGIKLDP 415
 Db 357 DLFENKPFLLIHDSTDTPLFVGKWDMP 385

RESULT 12
 JX0129
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 15-Sep-2003
 C:Accession: JX0129; B25420; S15905; S23673; S31367
 R:Suzuki, Y.; Yamamoto, K.; Sinohara, H.
 J. Biochem. 108, 344-346, 1990
 A:Title: Molecular cloning and sequence analysis of full-length cDNA coding for mouse cd
 A:Reference number: JX0129; MUID:91115777; PMID:2277027
 A:Accession: JX0129
 A:Molecule type: DNA
 A:Residues: 1-418 <SUZ>
 A:Cross-references: GB:D00725; NID:g220387; PIDN:BAA06627.1; PID:g220388
 A:Accession: A38826
 A:Molecule type: protein
 A:Residues: 30-48 <SUZ>
 R:Hill, R.E.; Shaw, P.H.; Boyd, P.A.; Baumann, H.; Hastie, N.D.
 Nature 311, 175-177, 1984
 A:Title: Plasma protease inhibitors in mouse and man: divergence within the reactive cen
 A:Reference number: A93340; MUID:84295637; PMID:6547997
 A:Accession: B25420
 A:Molecule type: mRNA
 A:Residues: 'V', 205-346, 'T', 348-418 <HIL>
 R:Ohkubo, K.; Ogata, S.; Misuma, Y.; Takami, N.; Sinohara, H.; Ikehara, Y.
 Biochem. J. 276, 337-342, 1991
 A:Title: Cloning, structure and expression of cDNA for mouse contraspin and a related pr
 A:Reference number: S15905; MUID:91264784; PMID:2049055
 A:Accession: S15905
 A:Molecule type: mRNA
 A:Residues: 1-83, 'R', 85-418 <OHK>
 A:Cross-references: EMBL:X55147; NID:g50441; PIDN:CAA38948.1; PID:g50442
 A:Accession: S23673
 A:Molecule type: protein
 A:Residues: 22-41, 67-83, 156-176, 218-227, 'X', 229-235; 315-334 <OGN>
 R:Yoshida, K.; Suzuki, Y.; Sinohara, H.
 submitted to the EMBL Data Library, November 1990
 A:Description: Nucleotide and deduced amino acid sequences of contraspin from C57bl/6 m
 A:Reference number: S31367
 A:Accession: S31367
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-67, 'Q', 69, 'K', 71-192, 'K', 194-199, 'DG', 202-249, 'A', 251-303, 'S', 305-319, 'D',
 A:Cross-references: EMBL:X56786; NID:g54172; PIDN:CAA40106.1; PID:g54173
 C:Comment: Contraspin is a plasma glycoprotein.
 C:Superfamily: Serpin
 C:Keywords: Glycoprotein; serine proteinase inhibitor
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-29/Domain: propeptide #status predicted <PRO>
 F:30-418/Product: contraspin #status experimental <MAT>
 F:39,105,185,270/Binding site: carbonyl site: carbonyl (Asn) (covalent) #status predicted

Query Match 19.7%; Score 420; DB 2; Length 418;
 Best Local Similarity 30.9%; Pred. No. 2.4e-23;
 Matches 118; Conservative 80; Mismatches 154; Indels 30; Gaps 12;

QY 54 LAAAVSNGFYDLYVRSSMPTTNVLLSPSVATLSALSGAEQRTESIIRALYDIL 113
 Db 48 LASVNTDFAFLYKXKALKNPDNIWFSPLSISAALVSLGAKGTMEILEGLKFNLT 107
 QY 114 SSP--DIHGTYKELDTVTAP--QKNLKSASRIVFEKLRKSSFFVAPLEKSYGTRPRVL 169
 Db 108 ETEADHQFGNQLSLSQEPDQDQINIGNAMFIEKDIQILAEF---HEK---TEALYQ 161

QY 170 TGNPRDLQOE-----INNWTQACMKGLARSTKEIPDEISILLGVAFKQGWVTKFD 222
 Db 162 TEAFTADPOQTEAKNLINDYVSNQTOGMKELISELDELTMLVNVVIYFKGKWKISFD 221
 QY 223 SRKTSLEDFYLDERTVVRPMNSDPKAVLRVGLDSDLSCKIAQLPLTGSMSIIFPLPLK 282
 Db 222 PQDTFSEFYLDKESVQVPMKMLLTTRHPRDEELSCSVLELKLYTCGNASALLLPDQ- 280
 QY 283 TQNLTLIEESLTSFIHIDRELKTQV-AVLTVPKLKSVEGEVTKS-LQEMKLOSLF-D 339
 Db 281 -GRMQQVEASLQPETLRKWRKTLFPSQIEELNLPKFSIASNYRLEEDVLPENGKEVTE 339
 QY 340 SPDFSKIT-GKPIKLTQVEHRAFGFENNEDG---AGTTPSPGLOPAHLTFPLDYLHNOFP 394
 Db 340 QADLSGITETKLSVSQVVKAVLDVAETGTETAAATGVIGIRKAILP---AVHFRNPP 396
 QY 395 IFVLRDPTDGTGALLFGIKLDP 416
 Db 397 LEVIYHTSAQSILFMKVNPK 418

RESULT 13
 S31507
 C:Species: Apodemus sylvaticus (European woodmouse)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 15-Sep-2003
 C:Accession: S31507
 R:Ingilis, J.D.; Lee, M.; Hill, R.E.
 submitted to the EMBL Data Library, December 1992
 A:Reference number: S31505
 A:Accession: S31507
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <ING>
 A:Cross-references: EMBL:X69833; NID:g49418; PIDN:CAA49487.1; PID:g49419
 C:Superfamily: Serpin

Query Match 19.7%; Score 419.5; DB 1; Length 418;
 Best Local Similarity 28.1%; Pred. No. 2.6e-23;
 Matches 112; Conservative 92; Mismatches 163; Indels 31; Gaps 11;

QY 38 ALVREEDFFKVPVKNLAAVSNFGYDLYVRSSMPTTNVLLSPSVATLSALSGAE 97
 Db 31 AVQEDQNGTQVDSLTLASINTDFAFLYKELAKNPDKNIVFSPLSISAALVSLGAK 90
 QY 98 QRTESIIRALYDILISP--DIHGTYKELDTV--TAPQKNLKSASRIVFEKLRKSS 153
 Db 91 CNTLQELLEGKFNLTETPEADIHLGFRHLHMLSQSGKEEQINIAVSMFTEKHLQILAE 150
 QY 154 FVAPLEKSYGTRPRVLTCNPRDLQOE-----INNWTQACMKGLARSTKEIPDEISIL 206
 Db 151 FOEKVRSYLL--QAAFAFTA---DFQDADEARKFINDYRKETQCKIQIELSLDLVERTSMV 204
 QY 207 LLGVAHFKQGWVTKFDGRKTSLEDFYLDERTVVRPMNSDPKAVLRVGLDSDLSCKIAQL 266
 Db 205 LVNVIYFKGKMKMPDPRVTLKSEFYLDKESVQVPMKMLIEDLTPYFRDEELSCSVL 264
 QY 267 PLTGSMSIIFPLPKVQTNLTIEESLTSFIHIDRELKTQV-AVLTVPKLKSVEGEV 325
 Db 265 KYIGNASALFLPDQ--GRTEQVEASLQPETLRKWKDSLPRKIDLLYLPKFLVSTDYSL 322
 QY 326 TKSIQEMKLOSLFDS-PDFSKITG-KPIKLTQVEHRAFGFENNEDGAGTTPSPGLOPAHLT 383
 Db 323 EDVLSELGIRKEVFAQADLSRVGTGKLSVSQVVKAVLDVAETGTETAAATGVIGIRKAILP 385
 QY 384 F-----PLDYHLNQPFIVLRDPTDGTGALLFGIKLDP 415
 Db 380 FRSGRVPTMTVRPRPRFLMVVSVHTGVSILFLAKVTNP 417

RESULT 14

TIBA

alpha-1-antitrypsin precursor - baboon (fragment)

N;Alternate names: alpha-1-proteinase inhibitor
C;Species: Papio sp. (baboon)
C;Date: 02-Apr-1992 #sequence_revision 02-Apr-1982 #text_change 15-Sep-2003
C;Accession: A01248
R;Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Da
Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A;Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.
A;Reference number: A01248; MUID:82082539; PMID:7031661
A;Accession: A01248
A;Molecule type: mRNA
A;Residues: 1-409 <KUR>
A;Cross-references: GB:J00321; NID:G176561; PIDN:AAA3377.1; PID:G176562
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
isin.
C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-409/Product: alpha-1-antitrypsin #status predicted <MAR>
F;61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;373/Inhibitory site: Met (elastase, collagenase) #status predicted
Query Match 19.6%; Score 418; DB 1; Length 409;
Best Local Similarity 28.1%; Pred. No. 3.3e-23;
Matches 117; Conservative 87; Mismatches 187; Indels 26; Gaps 10;
QY 13 LLGHSSCONPASPEEGSPDSTGALVEBEDPFFK--VPVNKLAASVNFYDLYRVS 70
Db 2 LLAGLCCLLFGSLAE---DPQGAQKDTTPHDQNHPLINKTPSLAEFAFSLYRQLA 57
QY 71 SMSPTTNVLSPLSVAALSALSGAORTESIHRALYDLSPPD--IHGYKELLDT 128
Db 58 HQSNSTNIFPSPVSIATAFAMLSLGTADTHSEILEGNFNLTETPEAQVHEGFQELLRT 117
QY 129 VTAP--QKNLSASRIPEKLRKIKSFVAPLEKSYGRP-RVLTGNPRDLQBINNVQ 185
Db 118 LNKDPSQLQLTGNGFLNKLKVVDFLEVDKVLNLYSEAFNFEDEAKQINNYE 177
QY 186 AQMGKGLARSTKEIPDEISILLGVAFKQGVTKFDSRKTSLDEFDYLDERTVRVPMMS 245
Db 178 KGTQGVVDLVKELDRDVFALVNYIFPKGWERPFVEATEEEDFHDQATTVKVPMMR 237
QY 246 DPKAVLRGLSDLSCK-----IAQLPLTGSMSIIFPLKVTQNTLIEESLTSEIHD 300
Db 238 -----RLGMFNHYHCEKLSWMLMKYLGNATAIFLEPDE--GKLOHLENELTHDILT 289
QY 301 IDRELKTVQAVLTVPKLSVEGEVTKSLQMKLQSLF--DSPDFSKIT-GKPIKLTQVEH 358
Db 290 FLENENRSANLHLPKLAITGYDLKTVLGHGKITVPSNGADLSGVTEADAPLKSXAVH 349
QY 359 PAGFPWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFFIVLRDRTDTGALLFIGKILDP 415
Db 350 KAVLTIDEKGTGAAGAFLEAIPKSIPEPVKFNKPFVFLMTEQNTKSPFLFIGKVNP 406
RESULT 15
S23675
contrapsin-related protein MC-7 precursor - mouse
N;Alternate names: serine proteinase inhibitor 2.4
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 15-Sep-2003
C;Accession: S23675; S21506; S15632; S19078; S21870
R;Ohkubo, K.; Ogata, S.; Misumi, Y.; Takami, N.; Sinohara, H.; Ikehara, Y.
Biochem. J. 276, 337-342, 1991
A;Title: Cloning, structure and expression of cDNA for mouse contrapsin and a related pr
A;Reference number: S15905; MUID:91264784; PMID:2049065
A;Accession: S23675
A;Molecule type: mRNA
A;Residues: 1-418 <CHK>
A;Cross-references: EMBL:X55148; NID:G50443; PIDN:CAA38949.1; PID:G50444
A;Experimental source: strain BAUB/c
R;Ingilis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31505

A;Accession: S31506
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 145-312, R', 314-418 <ING>
A;Cross-references: EMBL:X69832; NID:G54174; PIDN:CAA49486.1; PID:G54175
R;Ingilis, J.D.; Hill, R.E.
EMBO J. 10, 255-261, 1991
A;Title: The murine Spi-2 proteinase inhibitor locus: a multigene family with a hyperva
A;Reference number: S15628; MUID:91122031; PMID:1991447
A;Accession: S15632
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 355-418 <IN2>
A;Cross-references: EMBL:X56820
R;Ingilis, J.D.
submitted to the EMBL Data Library, December 1990
A;Reference number: S19078
A;Accession: S19078
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 355-390, L', 392-418 <IN3>
A;Cross-references: EMBL:X56820
C;Superfamily: Serpin
C;Keywords: glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-418/Product: contrapsin #status predicted <VAR>
F;104,184,269/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 19.6%; Score 418; DB 2; Length 418;
Best Local Similarity 28.8%; Pred. No. 3.4e-23;
Matches 119; Conservative 75; Mismatches 165; Indels 54; Gaps 11;
QY 27 EGSPDPDSTGALVEBEDPFFKVPVNKLAASVNFYDLYRVSMSPTNVLLSPLSVA 86
Db 37 ESGTPDPSLT-----LASINTDFAFSLYKELVLKNPKDNIVFSPLSIS 79
QY 87 TALSALSAGAEORTESIHRALYDLD--TSSPDHGTYSKELLDITVAP--QKNLSASRI 142
Db 80 AALAVSLGAKGNTLEEILEGLKFNLTETSEADIHQGFHLLQRLSQPEDQDQINIGNAM 139
QY 143 VFEKLRKIKSFVAPLEKSYGRPRVLTGNPRDLQD-----INNVOAQMKGLKARS 195
Db 140 FIEKDLQILAEFHEKARALYQTEAFT-----ADFQKPTAKNLINDYVSNQTQGMKEL 193
QY 196 TKEIPDEISILLGVAFKQGVTKFDSRKTSLDEFDYLDERTVRVPMMSDPKAVLRYL 255
Db 194 ISELDTDTLMVLVNYIFPKGWKISFPDQDTESEFYLDEKRSVKVPMKMFELTRHFR 253
QY 256 DSDLCKIAQLPLTGSMSIIFPLKVTQNTLIEESLTSEFIHDIDRELKTVQ-AVLTV 314
Db 254 DEELSCSVLELKYTGNASALFILPDQ--GRMQQVEASLQPETLRKWKWSLKTAKIGELYL 311
QY 315 PKLKLSYGEVTKSLQMKLQSLFD-SPDFSKITG-KPIKLTQVEHRAGFENEDCAGIT 372
Db 312 PFSISITDYNLKDILPELGIKEIFSKQADLSGITGKLSVSQVHVHKAULVDAETGEAA 371
QY 373 PSPG-----LQPAHLTFPLDYHLNQPFFIVLRDRTDTGALLFIGKILDP 416
Db 372 AATGTFIFGFSRRRLQMTVQF-----NRPFLMVISHTGVTTLFMAKVTPNK 418
Search completed: September 1, 2004, 11:18:16
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: September 1, 2004, 10:59:03 ; Search time 25 seconds
(without alignments)
870.613 Million cell updates/sec

Title: US-10-619-149-1

Perfect score: 2131
Sequence: 1 MQALVLLCTGALLGHSSQ.....RDTGTCALLFGKILDPGRP 418

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	100.0	418	1 PEDF HUMAN	P36955 homo sapien
2	1861	87.3	416	1 PEDF BOVIN	Q95121 bos taurus
3	1856.5	87.1	417	1 PEDF MOUSE	P97298 mus musculus
4	470	22.1	492	1 A2AP BOVIN	P28900 bos taurus
5	466.5	21.9	431	1 A2AP MOUSE	Q61247 mus musculus
6	456.5	21.4	491	1 A2AP HUMAN	P08697 homo sapien
7	455	21.0	410	1 COTR CAVPO	P22323 cavia porce
8	448	21.0	405	1 A1AS CAVPO	P22325 cavia porce
9	443	20.8	413	1 CPI3 RAT	P05544 rattus norv
10	440	20.6	403	1 A1AF CAVPO	P22324 cavia porce
11	430.5	20.2	416	1 CPI1 RAT	P05545 r contrapsi
12	429.5	20.2	413	1 ALMF TMSI	Q54757 tamias sibi
13	427	20.0	418	1 A1AT HUMAN	P01009 homo sapien
14	424.5	19.9	413	1 ALMS TMSI	Q54758 tamias sibi
15	424.5	19.9	413	1 ALST TMSI	Q54760 tamias sibi
16	421.5	19.8	413	1 ALST TMSI	Q54759 tamias sibi
17	420	19.7	418	1 COTR MOUSE	P07759 mus musculus
18	419.5	19.7	418	1 SI24 APOSY	Q60396 apodemus sy
19	418	19.6	409	1 A1AT PAPAN	P01010 papio anubi
20	415.5	19.5	406	1 CBG SATSC	P50451 salmisi sci
21	414	19.4	411	1 A1AT RAT	P17475 rattus norv
22	408.5	19.2	413	1 HP55 TMSI	Q09055 tamias sibi
23	408	19.1	413	1 A1AF RABIT	P23035 oryctolagus
24	406.5	19.1	418	1 CPI6 RAT	P09006 rattus norv
25	405.5	19.0	413	1 A1T5 MOUSE	Q00898 mus musculus
26	404	19.0	379	1 ILEU HORSE	P05619 equus cabal
27	403	18.9	416	1 A1AT BOVIN	P34955 bos taurus
28	403	18.9	417	1 KBP MOUSE	P29621 mus musculus
29	402.5	18.9	421	1 A1AT PIG	P50447 sus scrofa
30	401.5	18.8	412	1 A1AT CALCN	Q54763 callosiuru
31	396.5	18.6	423	1 RACT HUMAN	P01011 homo sapien
32	395.5	18.6	500	1 ICL HUMAN	P05155 homo sapien
33	395	18.5	405	1 CBG HUMAN	P08185 homo sapien

34	386	18.1	416	1 A1AT SHEEP	P12725 ovis aries
35	382	17.9	409	1 THEG RAT	P35577 rattus norv
36	381.5	17.9	410	1 A1AT DIDMA	Q03044 didelphis m
37	381.5	17.9	427	1 KAIN HUMAN	P23622 homo sapien
38	380.5	17.9	413	1 A1T1 MOUSE	P07758 mus musculus
39	380.5	17.9	413	1 A1T2 MOUSE	P22599 mus musculus
40	379.5	17.8	444	1 ZPI HUMAN	Q9uk55 homo sapien
41	379	17.8	383	1 CBG RABIT	P23775 oryctolagus
42	378.5	17.8	378	1 ILEU PIG	P80229 sus scrofa
43	378.5	17.8	413	1 A1T3 MOUSE	Q00896 mus musculus
44	377	17.7	430	1 CBG SHEEP	P49920 ovis aries
45	375.5	17.6	413	1 A1T4 MOUSE	Q00897 mus musculus

ALIGNMENTS

RESULT 1

PEDF_HUMAN
ID PEDF_HUMAN STANDARD; PRT; 418 AA.
AC P36955; Q96CTI; Q96R01; Q9BWA4;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF) (EPC-1).
GN SERPINF1 OR PEDF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=93165728; PubMed=8434014;
RA Steele F.R., Chader G.J., Johnson L.V., Tombran-Tink J.;
RT "Pigment epithelium-derived factor: neurotrophic activity and
RT identification as a member of the serine protease inhibitor gene
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1526-1530(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Yin B., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Vazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-332 FROM N.A.
RC TISSUE=Lung fibroblast;
RA Coljee V.W.;
RL Thesis (1996), Medical College of Pennsylvania / Philadelphia, U.S.A.
RN [5]

RP SEQUENCE OF 72-418 FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=93232057; PubMed=8473338;
RA Pignolo R.J., Cristofalo V.J., Rotenberg M.O.;
RX "Senescent WI-38 cells fail to express EPC-1, a gene induced in young
RT cells upon entry into the G0 state.";
RL J. Biol. Chem. 268:8949-8957(1993).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=94043097; PubMed=8226833;
RA Becerra S.P., Palmer I., Kumar A., Steele P.R., Shiloach J.,
RX Notario V., Chader G.J.;
RT "Overexpression of fetal human pigment epithelium-derived factor in
RT Escherichia coli. A functionally active neurotrophic factor.";
RL J. Biol. Chem. 268:23148-23156(1993).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=96029704; PubMed=7592790;
RA Becerra S.P., Sagasti A., Spinella P., Notario V.;
RT "Pigment epithelium-derived factor behaves like a noninhibitory
RT serpin. Neurotrophic activity does not require the serpin reactive
RT loop.";
RL J. Biol. Chem. 270:25992-25999(1995).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS).
RX MEDLINE=21457291; PubMed=11562499;
RA Simonovic M., Gettins F.G.W., Voiz K.;
RT "Crystal structure of human PEDF, a potent anti-angiogenic and neurite
RT growth-promoting factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:11131-11135(2001).
RN [9]
RP VARIANT THR-72.
RX MEDLINE=93329357; PubMed=10398730;
RA Koeneke R., Pina A.L., Loyer M., Davidson J., Robitaille J.,
RA Maumenee I., Tombran-Tink J.;
RT "Four polymorphic variations in the PEDF gene identified during the
RT mutation screening of patients with Leber congenital amaurosis.";
RL Mol. Vision 5:10-16(1999).
RN [10]
RP FUNCTION: NEUROTROPHIC PROTEIN; INDUCES EXTENSIVE NEURONAL
CC DIFFERENTIATION IN RETINOBLASTOMA CELLS. POTENT INHIBITOR OF
CC ANGIOGENESIS. AS IT DOES NOT UNDERGO THE S (STRESSED) TO R
CC (RELAXED) CONFORMATIONAL TRANSITION CHARACTERISTIC OF ACTIVE
CC SERPINS, IT EXHIBITS NO SERINE PROTEASE INHIBITORY ACTIVITY.
CC [11]
RP SUBCELLULAR LOCATION: Secreted.
CC [12]
RP TISSUE SPECIFICITY: RETINAL PIGMENT EPITHELIAL CELLS.
CC [13]
RP DEVELOPMENTAL STAGE: EXPRESSED IN QUIESCENT CELLS.
CC [14]
RP DOMAIN: THE N-TERMINAL (AA 44-121) EXHIBITS NEURITE OUTGROWTH-
CC INDUCING ACTIVITY. THE C-TERMINAL EXPOSED LOOP (AA 382-418)
CC IS ESSENTIAL FOR SERPIN ACTIVITY.
CC [15]
RP SIMILARITY: Belongs to the serpin family.
CC [16]
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CC or send an email to license@isb-sib.ch).
CC [17]
RP EMBL; M76979; AAA60058.1; -;
DR EMBL; AF400442; AAK92491.1; -;
DR EMBL; BC000522; AAK00522.1; -;
DR EMBL; BC013984; AAH13984.1; -;
DR EMBL; U57450; AAB38685.1; -;
DR EMBL; U57445; AAB38685.1; JOINED.
DR EMBL; U57446; AAB38685.1; JOINED.
DR EMBL; U57447; AAB38685.1; JOINED.
DR EMBL; U57448; AAB38685.1; JOINED.
DR EMBL; U57449; AAB38685.1; JOINED.
DR EMBL; M90439; AAA93524.1; -;
DR PIR; A47281; A47281.
DR PDB; 1IMV; 03-OCT-01.
DR Genew; HGNC:8824; SERPINF1.

DR MIM; 172860; -;
DR GO; GO:0004867; F:serine protease inhibitor activity; TAS.
DR GO; GO:0004868; F:serpin; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Glycoprotein; Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 15
FT CHAIN 16 418
FT ACT_SITE 382 382
FT CARBOHYD 285 285
FT VARIANT 72 72
FT CONFLICT 97 98
FT CONFLICT 132 132
FT HELIX 45 48
FT HELIX 50 72
FT TURN 74 75
FT STRAND 78 80
FT HELIX 82 92
FT HELIX 93 95
FT HELIX 98 107
FT TURN 108 109
FT HELIX 110 112
FT HELIX 118 129
FT TURN 130 130
FT TURN 132 133
FT STRAND 136 144
FT TURN 146 147
FT HELIX 152 162
FT STRAND 167 168
FT HELIX 173 187
FT TURN 188 190
FT STRAND 205 214
FT STRAND 217 219
FT HELIX 223 225
FT STRAND 227 232
FT STRAND 238 256
FT TURN 257 260
FT STRAND 261 268
FT TURN 269 271
FT STRAND 272 279
FT HELIX 287 290
FT TURN 291 292
FT HELIX 295 304
FT STRAND 306 315
FT STRAND 317 324
FT HELIX 326 330
FT TURN 331 335
FT HELIX 336 339
FT TURN 344 346
FT STRAND 353 364
FT STRAND 368 370
FT STRAND 387 389
FT STRAND 394 400
FT TURN 401 403
FT STRAND 406 412
FT TURN 415 416
SQ SEQUENCE 418 AA; 46342 MW; 29B573A62EA51BE5 CRC64;
Query Match 100.0%; Score 2131; DB 1; Length 418;
Best Local Similarity 100.0%; Pred.No. 1.5e-148;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQALVLLCCTGALLCHSSCONPASPEEGSPDSTGALVEEDPFKVPVNLAAVSN 60
DB 1 MQALVLLCCTGALLCHSSCONPASPEEGSPDSTGALVEEDPFKVPVNLAAVSN 60
QY 61 FGDLVVRGRSMSPPTTNVLLSPVATLALSALSGAEQRTESIHRALYDYDLISSPDING 120

Db 61 FGVDLYRVRSMPTNNVLLSPVATLSALSGAERTESIHRALYDLISSPDH 120
Qy 121 TYKELDTVTAPQNKLSASRIIVFKKLRKSSFVAPLEKSYGTRVLTGNPRDLQEI 180
Db 121 TYKELDTVTAPQNKLSASRIIVFKKLRKSSFVAPLEKSYGTRVLTGNPRDLQEI 180
Qy 181 NNWVQAMQKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLEDFYLDERTYR 240
Db 181 NNWVQAMQKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLEDFYLDERTYR 240
Qy 241 VPMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSEFIHD 300
Db 241 VPMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSEFIHD 300
Qy 301 IDRELKTVQAVLTPKLSYEVEGTVKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 360
Db 301 IDRELKTVQAVLTPKLSYEVEGTVKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 360
Qy 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTGTGALLFGKILDRGP 418
Db 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTGTGALLFGKILDRGP 418

RESULT 2

PEDF_BOVIN STANDARD; PRT; 416 AA.
ID PEDF_BOVIN
AC Q95121;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF).
GN SERPINF1 OR PEDF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retinal pigment epithelium;
RA Perez-Medavilla L., Chew C., Campochiaro P., Zack D.J.,
RA Becerra S.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Singh V.K., Chader G.J., Rodriguez I.R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 21-47 AND 380-399.
RC TISSUE=Eye;
RX MEDLINE=96029704; PubMed=7592790;
RA Becerra S.P., Segasti A., Spinella P., Notario V.;
RT "Pigment epithelium-derived factor behaves like a noninhibitory
RT serpin. Neurotrophic activity does not require the serpin reactive
RT loop.";
RL J. Biol. Chem. 270:25992-25999 (1995).
CC -!- FUNCTION: NEUROTROPHIC PROTEIN; INDUCES EXTENSIVE NEURONAL
CC DIFFERENTIATION IN RETINOBLASTOMA CELLS. POTENT INHIBITOR OF
CC ANGIOGENESIS. AS IT DOES NOT UNDERGO THE S (STRESSED) TO R
CC (RELAXED) CONFORMATIONAL TRANSITION CHARACTERISTIC OF ACTIVE
CC SERPINS, IT EXHIBITS NO SERINE PROTEASE INHIBITORY ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: RETINAL PIGMENT EPITHELIAL CELLS. LOCATED IN
CC THE INTERPHOTORECEPTOR MATRIX (IPM) WHICH IS BETWEEN THE RETINAL
CC PIGMENT EPITHELIUM AND THE NEURAL RETINA.
CC -!- DOMAIN: THE N-TERMINAL (AA 42-139) EXHIBITS NEURITE OUTGROWTH-
CC INDUCING ACTIVITY. THE C-TERMINAL EXPOSED LOOP (AA 380-416)
CC IS ESSENTIAL FOR SERPIN ACTIVITY.
CC -!- SIMILARITY: Belongs to the serpin family.
CC -----
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CC -----
DR EMBL; U48229; AAC4856.1; -.
DR EMBL; AF017059; AAC05732.1; -.
DR HSSP; P36955; 1MV.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 416
FT CARBOHYD 283 283
FT ACT_SITE 380 380
FT CONFLICT 21 21
FT CONFLICT 46 46
SQ SEQUENCE 416 AA; 46229 MW; F6C76B6A4C9A4ECA CRC64;

Query Match 87.3%; Score 1861; DB 1; Length 416;
Best Local Similarity 87.5%; Pred. No. 8.4e-129;
Matches 365; Conservative 23; Mismatches 27; Indels 2; Gaps 1;
Qy 1 MOALVLLICIGALGHSSCONPASPPEGSPDPSTGALVEEDPFFKVPVKNKLAAYSN 60
Db 1 MOALVLLWTGALLGFGRCQAGQ--EAGSLTPESTGAPVEEDPFFKVPVKNKLAAYSN 58
Qy 61 FGVDLYRVRSMPTNNVLLSPVATLSALSGAERTESIHRALYDLISSPDH 120
Db 59 FGVDLYRVRSGESPANVLLSPVATLSALSGAERTESIHRALYDLISSPDH 118
Qy 121 TYKELDTVTAPQNKLSASRIIVFKKLRKSSFVAPLEKSYGTRVLTGNPRDLQEI 180
Db 119 TYKDLASVTAPQNKLSASRIIVFKKLRKSSFVAPLEKSYGTRVLTGNPRDLQEI 178
Qy 181 NNWVQAMQKGLARSTKEIPDEISILLGVAFKQGWTKFDSRKTSLEDFYLDERTYR 240
Db 179 NNWVQAMQKGVARSTREMPSEISILLGVAFKQGWTKFDSRKTSLEDFYLDERTYR 238
Qy 241 VPMSDPKAVLRGLDSDLSCKIAQLPLTGSMSIIFPLPKVTQNTLIEESLTSEFIHD 300
Db 239 VPMSDPQAVLRGLDSDLNCKIAQLPLTGSTSIFFLPKVTQNTLIEESLTSEFIHD 298
Qy 301 IDRELKTVQAVLTPKLSYEVEGTVKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 360
Db 299 IDRELKTVQAVLTPKLSYEVEGTVKSLQEMKLSLFDSPDPSKITGPKIKLTQVEHRA 358
Qy 361 GFENWEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTGTGALLFGKILDRGP 417
Db 359 GFENWEDGAGTNSPFGVQPARLTFPLDYHLNQPFIFVLRDTGTGALLFGKILDRGP 415

RESULT 3

PEDF_MOUSE STANDARD; PRT; 417 AA.
ID PEDF_MOUSE
AC P97298;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF) (stromal cell-
DE derived factor 3) (SDF-3).
GN SERPINF1 OR PEDF OR SDF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97092876; PubMed=8938438;
RX Shirozu M., Tada H., Tashiro K., Nakamura T., Lopez N.D., Nazarea M.,

RA Hamada T., Sato T., Nakano T., Honjo T.;
RT "Characterization of novel secreted and membrane proteins isolated by
RL the signal sequence trap method.";
RL Genomics 37:273-280(1996).
CC -!- FUNCTION: NEUTROPHILIC PROTEIN; INDUCES EXTENSIVE NEURONAL
CC DIFFERENTIATION IN RETINOLASTOMA CELLS. POTENT INHIBITOR OF
CC ANGIOGENESIS. AS IT DOES NOT UNDERGO THE S (STRESSED) TO R
CC (RELAXED) CONFORMATIONAL TRANSITION CHARACTERISTIC OF ACTIVE
CC SERPINS, IT EXHIBITS NO SERINE PROTEASE INHIBITORY ACTIVITY (BY
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the serpin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D50460; BAA09051.1; -;
CC HSP; P36955; 11MV.
CC MGD; MG1.108080; Serpinf1.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Glycoprotein; Signal.
CC SIGNAL 1 15 POTENTIAL.
CC CHAIN 16 417 PIGMENT EPITHELIUM-DERIVED FACTOR.
CC ACT SITE 381 381 REACTIVE BOND (BY SIMILARITY).
CC CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 417 AA; 46204 MW; ED68605B6A74D35 CRC64;
CC -----
CC Query Match 87.1%; Score 1856.5; DB 1; Length 417;
CC Best Local Similarity 86.5%; Pred. No. 1.8e-128;
CC Matches 360; Conservative 34; Mismatches 19; Indels 3; Gaps 2;
CC -----
CC 1 MQALVLLCTGALLGHSSCON-PASPPREGSPDDSTGALVEEDPFFKVPVKNKAAAVS 59
CC 1 MQALVLLMTGALLGHSSQNVPS--SEGPSVPDSTGEPVEEDPFFKVPVKNKAAAVS 58
CC 60 NFGVLDYRVSSSPTNNVLLSPLSVATALSALSGAEORTESIHRALYDILSSPDTH 119
CC 59 NFGYDLYRLSSASPTGNVLLSPLSVATALSALSGAEHTSVIHRALYDILINPDH 118
CC 120 GTYKELDTVTAPQKNLKSASRIYVFEKKLRKSSFVAPLEKSYGTRPVLTGNPRLDLQ 179
CC 119 STYKELLASVTAPEKNLKSASRIYVFEKKLRVKSFFVAPLEKSYGTRPVLTGNPRVDLQ 178
CC 180 INNWQAQMGKGLARSTKEIPDSITLLGVAFHFGQWTKFDSRKTSLDEYVLEERTV 239
CC 179 INNWQAQMGKGLARSTREMPSSALSILLGVAFHFGQWTKFDSRKTLLQDPHLDEDTV 238
CC 240 RVPWMDPKAVLYGLDSDLSCKIAQLPTGSMISIFFLPKVTQNTLIEESLSETH 299
CC 239 RVPWMDPKAILYGLDSDLNCKIAQLPTGSMISIFFLPVAVTQNTLIEESLSETH 298
CC 300 DIDRELKTQAVLTVPKLYSVEGVTKSLQENKLSQSFDSFKITGPKLTQVEHR 359
CC 299 DIDRELKTQAVLTVPKLYSFEGETKSLQDMKLSQSFDSFKITGPKLTQVEHR 358
CC 360 AGPEWNEGAGTTPSPGLPAHLTFPLDYHLNLPFFVLVLDTDGTGALLFGKILDP 415
CC 359 AAEWNEEGGSSPSGLQVRLTFFPLDYHLNLPFLVLRDITGALLFGKILDP 414
CC -----
CC RESULT 4
CC A2AP BOVIN STANDARD; PRT; 492 AA.
CC ID -A2AP BOVIN
CC AC P2880;
CC DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI)
DE (Alpha-2-AP).
GN SERPINF2 OR PLI.
OS Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94229242; PubMed=7513654;
RA Christensen S., Berglund L., Sottrup-Jensen L.;
RT "Primary structure of bovine alpha 2-antiplasmin.";
RL FEBS Lett. 343:223-228(1994).
RN [2]
RP SEQUENCE OF 23-45 AND 374-410.
RC TISSUE=Plasma;
RX MEDLINE=93050153; PubMed=1385210;
RA Christensen S., Sottrup-Jensen L.;
RT "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence.";
RL FEBS Lett. 312:100-104(1992).
CC -!- FUNCTION: The major targets of this inhibitor are plasmin and
CC trypsin, but it also inactivates chymotrypsin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
CC -----
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CC -----
CC EMBL; X78436; CAAS5200.1; -;
CC PIR; S43977; S43977.
CC HSP; P01008; IANT.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Acute phase; Serine protease inhibitor; Serpin; Plasma; Signal;
CC Glycoprotein; Sulfation.
CC SIGNAL 1 22
CC CHAIN 23 492 ALPHA-2-ANTIPLASMIN.
CC ACT SITE 404 405 REACTIVE BOND (FOR PLASMIN).
CC ACT SITE 405 406 REACTIVE BOND (FOR CHYMOTRYPSIN).
CC DISULFID 71 144 BY SIMILARITY.
CC MOD RES 485 485 SULFATION (BY SIMILARITY).
CC CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 28 28 T -> Q (IN REF. 2).
CC CONFLICT 40 40 Q -> P (IN REF. 2).
CC CONFLICT 43 43 Q -> E (IN REF. 2).
CC SEQUENCE 492 AA; 54710 MW; 075D6FC89B2DF5D CRC64;
CC -----
CC Query Match 22.1%; Score 470; DB 1; Length 492;
CC Best Local Similarity 30.2%; Pred. No. 7e-27;
CC Matches 120; Conservative 75; Mismatches 175; Indels 28; Gaps 7;
CC -----
CC 22 PASPEEG--SPDDSTGALVEEDPFFKVPVKNKAAAVSNFGYDLYRVSSSPTNNVL 79
CC 64 PKKAPEDCKLSPTPEQT-----RRLARMMWTFITDLFSLVAQSSTSPNLI 108
CC 80 LSPLSVALSALSGAEQRTESIHRALYDILSSPDTHGTYKELDTVTAPQKNLKS 139
CC 109 LSPLSVALSHLALGAQNQTLQRLKEVLHAD--SGPCLPHLLSRLCQDLGPCAFRL--A 164

RA Hirosawa S., Nakamura Y., Miura O., Sumi Y., Aoki N.;
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1612-1613(1989).
 RN [4]
 RP SEQUENCE OF 4-491 FROM N.A.
 RA MEDLINE=87109313; PubMed=2433286;
 RX Holmes W.E., Nelles L., Lijnen H.R., Collen D.;
 RT "Primary structure of human alpha 2-antiplasmin, a serine protease
 inhibitor (serpin).";
 RL J. Biol. Chem. 262:1659-1664(1987).
 RN [5]
 RP SEQUENCE OF 218-491 FROM N.A.
 RA MEDLINE=87137400; PubMed=3818581;
 RX Sumi Y., Nakamura Y., Aoki N., Sakai M., Muramatsu M.;
 RT "Structure of the carboxyl-terminal half of human alpha 2-plasmin
 inhibitor deduced from that of cDNA.";
 RL J. Biochem. 100:1399-1402(1986).
 RN [6]
 RP SEQUENCE OF 40-491.
 RA MEDLINE=87275946; PubMed=2440681;
 RX Lijnen H.R., Holmes W.E., van Hoef B., Wiman B., Rodriguez H.,
 RA Collen D.;
 RT "Amino-acid sequence of human alpha 2-antiplasmin.";
 RL Eur. J. Biochem. 166:565-574(1987).
 RN [7]
 RP SEQUENCE OF 40-43.
 RA MEDLINE=78023887; PubMed=21075;
 RX Wiman B., Collen D.;
 RT "Purification and characterization of human antiplasmin, the
 fast-acting plasmin inhibitor in plasma.";
 RL Eur. J. Biochem. 78:19-26(1977).
 RN [8]
 RP SEQUENCE OF 28-52.
 RA TISSUE=Plasma;
 RX MEDLINE=93050153; PubMed=1385210;
 RA Christensen S., Sottrup-Jensen L.;
 RT "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence.";
 RL FEBS Lett. 312:100-104(1992).
 RN [9]
 RP ACTIVE SITES.
 RA MEDLINE=88290696; PubMed=2456616;
 RX Potempa J., Shieh B.-H., Travis J.;
 RA "Alpha-2-antiplasmin: a serpin with two separate but overlapping
 reactive sites.";
 RL Science 241:699-700(1988).
 RN [10]
 RP DISULFIDE BOND.
 RA MEDLINE=97270633; PubMed=9169621;
 RX Christensen S., Vainickova Z., Thøgersen I.B., Olsen E.H.,
 RA Engdahl J.J.;
 RT "Assignment of a single disulphide bridge in human alpha2-antiplasmin:
 implications for the structural and functional properties.";
 RL Biochem. J. 323:847-852(1997).
 RN [11]
 RP SEQUENCE OF 481-491, AND SULFATION.
 RA MEDLINE=87137577; PubMed=2434496;
 RX Hørtin G., Pok K.F., Tøren P.C., Strauss A.W.;
 RT "Sulfation of a tyrosine residue in the plasmin-binding domain of
 alpha 2-antiplasmin.";
 RL J. Biol. Chem. 262:3082-3085(1987).
 RN [12]
 RP VARIANT ALPHA-2-PLASMIN INHIBITOR DEFICIENCY GLU-176 DEL.
 RA MEDLINE=90036902; PubMed=2572590;
 RX Mura O., Sugahara Y., Aoki N.;
 RT "Hereditary alpha 2-plasmin inhibitor deficiency caused by a
 transport-deficient mutation (alpha 2-PI-Okinawa). Deletion of Glu176
 by a trinucleotide deletion blocks intracellular transport.";
 RL J. Biol. Chem. 264:18213-18219(1989).
 RN [13]
 RP VARIANT ALPHA-2-PLASMIN INHIBITOR DEFICIENCY MET-411, AND VARIANTS
 VAL-27; TRP-33 AND LYS-434.
 RX MEDLINE=20051147; PubMed=10593218;
 RA Lind B., Thørsen S.;
 RT "A novel missense mutation in the human plasmin inhibitor

RT (alpha2-antiplasmin) gene associated with a bleeding tendency.";
 RL Br. J. Haematol. 107:317-322(1999).
 CC -!- FUNCTION: The major targets of this inhibitor are plasmin and
 CC trypsin, but it also inactivates chymotrypsin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -!- DISEASE: Defects in SERPINF2 are the cause of alpha-2-plasmin
 CC inhibitor deficiency (MIM:262850); a disease resulting in severe
 CC hemorrhagic diathesis.
 CC -!- SIMILARITY: Belongs to the serpin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 DR EMBL; D00116; BAA00070.1; -;
 DR EMBL; D00174; BAA00124.1; -;
 DR EMBL; M20786; AAA51554.1; -;
 DR EMBL; M20782; AAA51554.1; JOINED.
 DR EMBL; M20783; AAA51554.1; JOINED.
 DR EMBL; M20784; AAA51554.1; JOINED.
 DR EMBL; M20785; AAA51554.1; JOINED.
 DR EMBL; J02654; AAA35543.1; -;
 DR PIR; A31402; ITHU42.
 DR HSP; O35684; LJJO.
 DR SWISS-2DPAGE; P08697; HUMAN.
 DR Genew; HGNC:9075; SERPINF2.
 DR MIM; 262850; -;
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.
 DR GO; GO:0004868; F:serpin; TAS.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Acute phase; Serine protease inhibitor; Serpin; Plasma; Signal;
 KW Glycoprotein; Sulfation; Polymorphism; Disease mutation.
 FT SIGNAL 1 27
 FT PROPEP 28 39
 FT CHAIN 40 491
 FT ACT_SITE 403 404
 FT ACT_SITE 404 405
 FT CROSSLNK 41 41
 FT
 FT DISULFID 70 143
 FT MOD_RES 484 484
 FT CARBOHYD 126 126
 FT CARBOHYD 295 295
 FT CARBOHYD 309 309
 FT CARBOHYD 316 316
 FT VARIANT 27 27
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 FT VARIANT 33 33
 FT VARIANT 176 176
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 FT VARIANT 411 411
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 FT VARIANT 434 434
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 FT CONFLICT 49 49
 FT CONFLICT 105 105
 FT CONFLICT 289 289
 FT CONFLICT 408 408
 FT CONFLICT 455 455

SQ SEQUENCE 491 AA; 54565 MW; 385A1C90E91A63CB CRC64;

Query Match 21.4%; Score 456.5; DB 1; Length 491;
Best Local Similarity 28.4%; Pred. No. 6.8e-26;
Matches 127; Conservative 86; Mismatches 181; Indels 53; Gaps 11;

Qy 5 VLLICIGALHSCQNPAS-----PPEE-----GSPDPSTGAL--- 39
Db 7 LLVLSWSCLOQPCSVFSPVAMEPLGRQLTSGPNQEQVSLTLIKGNQPGQGTALKSP 66

Qy 40 --VEEDPPFKVP--VNKLAAAVSNFGDLYRVSSMSPTTNVLLSPLSVATLSALSLG 95
Db 67 PGVCSRDP---TPQTHRLARAMWAFADLSVAQSTPCPNLLSPLSVALLSHLAG 123

Qy 96 AE-----QRTESIIRALYYDILISPDHGTGTYKELLDVTAPQKNLKSASRIVPEKLR 151
Db 124 AQNHTLQRLQVLHAG-----SGPCLPHLLSRLCQDLGFGAFRL--AARMYLQKGPPK 175

Qy 152 SSFVAPLEKSYGTRPRVLTGNPRDLQEIINNVQAQMKGLARSTKIPDEISILLGVA 211
Db 176 EDFLEQSEQLFGAKPVSLTGQEDDLANINQWKEATGKIQEFLSGLPEDTVLLLNAI 235

Qy 212 HFKQGWTKFDSRKTSLDEDFYLDERTVRVPMSPDKAVLYRGDLSCKIAQLPTGS 271
Db 236 HFQGFWRNKFPDPSLTQRDSFHLDEQFTVPVEMMQARTYPLRWFLLEQPEIQVAHFPPKNN 295

Qy 272 MSIIFFPLKVTQNTLIEESLSEFTHD---IDRELKTQVAVLTVPKLSYGEVTKS 328
Db 296 MSFVVLVTPHEWNVQSLANLSDTLHPVLVWRPTK-----VRLPKLYLKQMDLVAT 350

Qy 329 LQEMKLSLSPSPFCKITGPVKILTOVEHRAGFENWEDGAGTTPSPGLOPAHLTFPLDY 388
Db 351 LSQGLQELFQAPDLRGISEQSLVSGVQHSITLSEVGVAAATSIAMRSLS-SF 409

Qy 389 HLNQPFVPLRDTDTGALLFGKILDP 415
Db 410 SVNRPFLEFIEDTTGLPLFVGVSRNP 436

RESULT 7

COTR_CAVPO STANDARD; PRT; 410 AA.

ID ALIAS_CAVPO STANDARD; PRT; 405 AA.

AC P22323;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-SEP-2003 (Rel. 41, Last annotation update)
DE Serine proteinase inhibitor A3K precursor (Contraapsin) (CP) (Serp
DE A3K).

OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-44.
RX MEDLINE=91093294; PubMed=1985973;
RA Suzuki Y., Yoshida K., Honda E., Sinohara H.;
RT "Molecular cloning and sequence analysis of cDNAs coding for guinea
RT pig alpha 1-antiproteinases S and F and contrapain.",
RL J. Biol. Chem. 266:928-932(1991).
CC -!- FUNCTION: CONTRAPAIN INHIBITS TRYPSIN-LIKE PROTEASES.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to the serpin family.

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or send an email to license@isb-sib.ch).

EMBL; M57269; AAA62806.1; --

DR PIR; C39088; C39088.
DR HSP; P01009; 8APl.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 410
FT ACT_SITE 374 375
FT CARBOHYD 62 62
FT CARBOHYD 99 99
FT CARBOHYD 162 162
FT CARBOHYD 229 229
FT CARBOHYD 263 263
SQ SEQUENCE 410 AA; 45599 MW; AS931286FA4605A0 CRC64;

Query Match 21.4%; Score 455; DB 1; Length 410;
Best Local Similarity 28.1%; Pred. No. 6.7e-26;
Matches 111; Conservative 101; Mismatches 159; Indels 24; Gaps 9;

Qy 37 GALVEE---EDPFKVPVNKLAAAVSNFGDLYRVSSMSPTTNVLLSPLSVATLSAL 92
Db 21 GIMAEIQVAVQSPSQHPSKVPKPSLAHFAHSHRVLTQOQSNITSFVSIATLAVY 80

Qy 93 SLGAEQRTESIIRALYYDILISPDHGTGTYKELLDVTAP--QKNLSASRIVPEKXL 148
Db 81 SLGAKGDTHTQILRSLEFNLTAEADHDGQFNLLHTLNRPHSEHQLTTGNGFLDQNL 140

Qy 149 RIKSSVABLEKSYGTRPRVLT--GNPRDLQEIINNVQAQMKGLARSTKIPDEISILL 207
Db 141 KLKEKESGVKTLTHAEAFPTNFSNPKAEKINAYVERGTQGVLDVYKDLGADTVLAL 200

Qy 208 LGVAHFKGQWTKFDSRKTSLDEDFYLDERTVRVPMSPDKAVLYRGDLSCKIAQ-- 265
Db 201 VNIIFRGKWKPEFDVKHTQEDFHDVANTTVKVPNMK-----QGVHKAHCSTIQSW 254

Qy 266 ---LPLTGSMSIIFPLKVTQNTLIEESLSEFTHDIDRELKTQVAVLTVPKLSYGE 322
Db 255 VLLLDYEGNVTALFLLPDE--GKMQLHELTLPFLVFKFLRKTETMPAYVPLKLSIGT 312

Qy 323 GEVTKLSIQEMKLSLSPFCKITGPVKILTOVEHRAGFENWEDGAGTTPSPGLOPA 380
Db 313 YDLKEVIRDLGINTNVFSGAADLSGITEDNPLKSLKGLHALLTIDEGTEAAATVLEAT 372

Qy 381 HLTFFPDYHLNQPFIFFLVLRDTDTGALLFGKILDP 415
Db 373 RTARPRLSPNKEFFFLIIDHSDTDTPLFVGVKMDP 407

RESULT 8

ALIAS_CAVPO STANDARD; PRT; 405 AA.

ID ALIAS_CAVPO STANDARD; PRT; 405 AA.

AC P22325;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-1-antiproteinase S precursor (Alpha-1-antitrypsin) (Alpha-1-
DE prteinase inhibitor) (AFS).
DE Cavia porcellus (Guinea pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-44 AND 75-93.
RX MEDLINE=91093294; PubMed=1985973;
RA Suzuki Y., Yoshida K., Honda E., Sinohara H.;
RT "Molecular cloning and sequence analysis of cDNAs coding for guinea
RT pig alpha 1-antiproteinases S and F and contrapain.",
RL J. Biol. Chem. 266:928-932(1991).
CC -!- FUNCTION: INHIBITS ELASTASE, CHYMOTRYPSIN, CATHEPSIN G, PLASMIN,
CC AND TRYPSIN.
CC -!- SUBCELLULAR LOCATION: Extracellular.

RT "Cloning and expression in *Escherichia coli* of full-length complementary DNA coding for human alpha 1-antitrypsin.";
DNA 2:255-264 (1983).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036645; PubMed=6387509;
RA Rosenber S., Barr P.J., Nejarian R.C., Hallelwell R.A.;
RT "Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-antitrypsin.";
RL Nature 312:77-80 (1984).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85047190; PubMed=6093867;
RA Long G.L., Chandra T., Woo S.L.-C., Davie E.W., Kurachi K.;
RT "Complete sequence of the cDNA for human alpha 1-antitrypsin and the gene for the S variant.";
RL Biochemistry 23:4828-4837 (1984).
[4]
RP SEQUENCE FROM N.A., AND DESCRIPTION OF VARIANT Z.
RX MEDLINE=87057257; PubMed=3491072;
RA Nukiwa T., Sacoh K., Brantly M.L., Ogushi F., Fells G.A.,
RT "Identification of a second mutation in the protein-coding sequence of the Z type alpha 1-antitrypsin gene.";
RL J. Biol. Chem. 261:15989-15994 (1986).
[5]
RP ERRATUM
RA Nukiwa T., Sacoh K., Brantly M.L., Ogushi F., Fells G.A.,
RT "Correction.";
RL J. Biol. Chem. 262:10412-10412 (1987).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE=85176977; PubMed=2985281;
RA Ciliberto G., Dente L., Cortese R.;
RT "Cell-specific expression of a transfected human alpha 1-antitrypsin gene.";
RL Cell 41:531-540 (1985).
[7]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
RT "Functional prediction of the coding sequences of 32 new genes deduced by analysis of cDNA clones from human fetal liver.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon, and Ovary;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RT "The human genome sequence: initial mapping and sequencing.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[9]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[10]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[11]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[12]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[13]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[14]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[15]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[16]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[17]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[18]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[19]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[20]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[22]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RP SEQUENCE OF 25-418.
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RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[26]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[27]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[28]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[29]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[30]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[31]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[32]
RP SEQUENCE OF 25-418.
RX MEDLINE=82220135; PubMed=7045697;
RA Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C.,
RT "The human alpha 1-antitrypsin gene: a review of the literature.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[33]<

RA Vaughan L., Boswell D.R.;
 RT "Structure and variation of human alpha 1-antitrypsin.";
 RL Nature 298:329-334(1982).
 RN [10]
 RP PRELIMINARY SEQUENCE OF 25-418.
 RA Chan S.K.;
 RT "The covalent structure of human alpha1-protease inhibitor.";
 RL Fed. Proc. 41:1016-1016(1982).
 RN [11]
 RP SEQUENCE OF 1-67; 196-255 AND 387-418 FROM N.A.
 RX MEDLINE=82220035; PubMed=6979715;
 RA Leicht M., Long G.L., Chandra T., Kurachi K., Kidd V.J., Mace M. Jr.,
 RA Davis E.W., Woo S.L.C.;
 RT "Sequence homology and structural comparison between the chromosomal
 RT human alpha 1-antitrypsin and chicken ovalbumin genes.";
 RL Nature 297:655-659(1982).
 RN [12]
 RP SEQUENCE OF 291-418 FROM N.A.
 RX MEDLINE=86005469; PubMed=3876243;
 RA Riley J.H., Bathurst I.C., Edbrooke M.R., Carrell R.W., Craig R.K.;
 RT "Alpha 1-antitrypsin and serum albumin mRNA accumulation in normal,
 RT acute phase and ZZ human liver.";
 RL FEBS Lett. 189:361-366(1985).
 RN [13]
 RP SEQUENCE OF 350-418 FROM N.A.
 RX MEDLINE=82082539; PubMed=7031661;
 RA Kurachi K., Chandra T., Friezen Degen S.J., White T.T.,
 RA Marchioro T.L., Woo S.L.C., Davie E.W.;
 RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
 RN [14]
 RP SEQUENCE OF 387-418 FROM N.A.
 RX MEDLINE=85225507; PubMed=3873938;
 RA Coutelle C., Speer A., Rogers J., Kalsheker N., Humphries S.,
 RA Williamson R.;
 RT "Construction and partial characterization of a human liver cDNA
 RT library.";
 RL Biomed. Biochim. Acta 44:421-431(1985).
 RN [15]
 RP CARBOHYDRATE-LINKAGE SITES ASN-70 AND ASN-271.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=84292309; PubMed=6332197;
 RA Loebmann H., Tokuda R., Deisenhofer J., Huber R.;
 RT "Human alpha 1-proteinase inhibitor. Crystal structure analysis of
 RT two crystal modifications, molecular model and preliminary analysis
 RT of the implications for function.";
 RL J. Mol. Biol. 177:531-556(1984).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=89221004; PubMed=2785270;
 RA Egh R., Loebmann H., Schneider M., Wiegand G., Huber R.,
 RA Laurell C.-B.;
 RT "The s variant of human alpha 1-antitrypsin, structure and
 RT implications for function and metabolism.";
 RL Protein Eng. 2:407-415(1989).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=20386623; PubMed=10933492;
 RA Elliott P.R., Fei X.Y., Dafforn T.R., Lomas D.A.;
 RT "Topography of a 2.0 A structure of alpha1-antitrypsin reveals targets
 RT for rational drug design to prevent conformational disease.";
 RL Protein Sci. 9:1274-1281(2000).
 RN [19]
 RP REVIEW.
 RX MEDLINE=89352843; PubMed=2669992;
 RA Kalsheker N.;
 RT "Alpha 1-antitrypsin: structure, function and molecular biology of

the gene.";
 RL Biosci. Rep. 9:129-138(1989).
 RN [20]
 RP REVIEW.
 RX MEDLINE=91315455; PubMed=1859394;
 RA Wu Y., Foreman R.C.;
 RT "The molecular genetics of alpha 1 antitrypsin deficiency.";
 RL Bioessays 13:163-169(1991).
 RN [21]
 RP DESCRIPTION OF VARIANT M2.
 RX MEDLINE=88324438; PubMed=2901226;
 RA Nukiwa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
 RT "Characterization of the gene and protein of the common alpha 1-
 RT antitrypsin normal M2 allele.";
 RL Am. J. Hum. Genet. 43:322-330(1988).
 RN [22]
 RP VARIANT M3 ASP-400.
 RX MEDLINE=90368097; PubMed=2394452;
 RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F.,
 RA Kalsheker N.A.;
 RT "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
 RT variant.";
 RL Hum. Genet. 85:381-382(1990).
 RN [23]
 RP VARIANT F CYS-247.
 RX MEDLINE=91241132; PubMed=2035534;
 RA Okayama H., Brantly M., Holmes M., Crystal R.G.;
 RT "Characterization of the molecular basis of the alpha 1-antitrypsin F
 RT allele.";
 RL Am. J. Hum. Genet. 48:1154-1158(1991).
 RN [24]
 RP VARIANT M-HEERLEN LEU-393.
 RX MEDLINE=89154435; PubMed=2784123;
 RA Hofker M.H., Nukiwa T., van Paassen H.M.B., Nelen M., Kramps J.A.,
 RA Klaasen E.C., Frants R.R., Crystal R.G.;
 RT "A Pro->Leu substitution in codon 369 of the alpha-1-antitrypsin
 RT deficiency variant PI M-Heerlen.";
 RN [25]
 RP Query Match 20.0%; Score 427; DB 1; Length 418;
 RP Best Local Similarity 28.2%; Pred. No. 7.8e-24;
 RP Matches 120; Conservative 93; Mismatches 170; Indels 42; Gaps 13;
 QY 13 LLGHSSQCNAPSPPEEGSPDSTGALV-----EEDPFFKVPVKNLAAAVNFGVDLY 66
 DB 11 LLAGCLCLVPVSLAE-----DPQDAAQKTDTSHHDDHPHF-----NKITNLAFAFSLY 62
 QY 67 RVRSSMPTTNVLSPLSVATALSALSGAERTESIIRALYDYLISPD--IHGTKE 124
 DB 63 RQLAHQSNSTNIPSPVSIATAFAMLSLGTADTHDEILEGLNFLTPEAQIHGFGQE 122
 QY 125 LLDVTWAP--QKXKXSASRIVFEKLIKSSVAPLEKSYGTRP-RVLTGNPLDLQELN 181
 DB 123 LLRTINQPDSQLQLTGNGFLSEGLKLVDFKLEDKVLYHSEAFVNFQDTEAKKQIN 182
 QY 182 NWQAOQMGKGLARSTKEIPDEISTILLGVAFHFGQWTKPDSRKTSLDEFLDEERTVY 241
 DB 183 DYVEKGTQGLKVDLVKELDRDTVFALVWYIFFKGKWERPEVKDTEEDFHVQVTVKV 242
 QY 242 PMSDPKAVLYRGLDSDLCK-----IAQLPLTGSMSIIFFLPKVTQNTLIESLT-- 294
 DB 243 PMMK-----RLGMFNTHQCKKLSSWVLLMKYLNATAIFFLPE--GKLQHLNELTHD 294
 QY 295 --SEFIHDIDRELKTVQAVLTVPKLLSYBGEVTKSLOEMKLSLF--DSPDFSKITGK-P 350
 DB 295 IITFLENERDR-----SASHLPKLSITGYDLKSVLGQGITKVSNGADLSGVTEEP 350
 QY 351 IKLTQVHRAGFEWNEDAGTTSPGLQPAHLTFPDYHNLNQPIFVLRDRTDTCALLFIG 410
 DB 351 LKLSKAVKAVLTIDKRGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIQNTKSPFLFMG 410
 QY 411 KILDP 415
 DB 411 KVNVP 415


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RESULT 14
ALMS_TAMSI STANDARD; PRT; 413 AA.
ID ALMS_TAMSI STANDARD; PRT; 413 AA.
AC OS4758;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-MS precursor.
OS Tamas sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamias.
CX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=94341474;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RA "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: Expressed in liver.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANITRYPSIN.
CC
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CC -----
CC EMBL; AB000547; BAA24417.1; -
CC HSP; P01009; IQLP.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 413
FT MOD_RES 25 25
FT CARBOHYD 65 65
FT CARBOHYD 102 102
FT CARBOHYD 165 165
FT CARBOHYD 266 266
FT ACT_SITE 377 378
FT SEQUENCE 413 AA; 45952 MW; 430374CA26EBAF08 CRC64;

Query Match 19.9%; Score 424.5; DB 1; Length 413;
Best Local Similarity 28.1%; Pred. No. 1.2e-23;
Matches 119; Conservative 101; Mismatches 169; Indels 33; Gaps 14;

QY 7 LLCIGALLGHSQCNAPSPPEGSPPDSTGALVEEDPFFKVPVKNLAASVNFYDLY 66
Db 9 LLLLAAL----SCLGPGSLAQDAQ---ETEASQDQEH-----ASHRIAPHLAEFALSLY 57
QY 67 RVSSMPTTNVLLSPLSVATASLSLGAQRTESIHRALYDYL--ISSPDHGTKE 124
Db 58 RVLARQNTNITFFSPVSIATAMLSLGTGKGTHTQILEGLDFNTEMAEADHGQFOH 117
QY 125 LLDVTVPAP--QKNLKSARIVFKKLIKSSVFAPLEKSYGTG--PRVLGTGNPRDLQRI 180
Db 118 LLQTLNRPNTQLQTSNGLFHQNKLKLLDKFLEDVKLSVSEAFPTNFT--NWEEARQOI 176
QY 181 NNWVQAMKGLARSTKEIPDEISILLGVAHFKGQWTKFDSRKTSLDFYLDERTVR 240
Db 177 NSYVEKGTQGIKVELVKELSDTVLNVNIFPKGKWLKPFNEHTREEDFHYDEATTVR 236

RESULT 15
ALSI_TAMSI STANDARD; PRT; 413 AA.
ID ALSI_TAMSI STANDARD; PRT; 413 AA.
AC OS4760;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-1-antitrypsin-like protein CM55-SI precursor.
OS Tamas sibiricus (Siberian chipmunk) (Asian chipmunk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Tamias.
CX NCBI_TaxID=64680;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=94341474;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RA "Expression of multiple alphas-1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- TISSUE SPECIFICITY: Expressed in liver.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-
CC ANITRYPSIN.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000549; BAA24419.1; -
CC HSP; P01009; 9API.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC SMART; SM00093; SERPIN; 1.
CC PROSITE; PS00284; SERPIN; 1.
CC Serpin; Serine protease inhibitor; Glycoprotein; Signal;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 413
FT MOD_RES 25 25
FT CARBOHYD 65 65
FT CARBOHYD 102 102
FT CARBOHYD 165 165
FT CARBOHYD 266 266
FT ACT_SITE 377 378
FT SEQUENCE 413 AA; 46202 MW; AB65A1D31B8CA2EC CRC64;

Query Match 19.9%; Score 424.5; DB 1; Length 413;
Best Local Similarity 28.1%; Pred. No. 1.2e-23;
Matches 119; Conservative 100; Mismatches 169; Indels 35; Gaps 13;

```


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OM protein - protein search, using sw model

Run on: September 1, 2004, 11:07:34 ; Search time 119 Seconds
(without alignments)
1108.291 Million cell updates/sec

Title: US-10-619-149-1
Perfect score: 2131
Sequence: 1 MQALVLLLCIGALLGHSSCQ.....RDTDTGALLFGIKILDRGP 418

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856.5	87.1	417	11	O70629
2	1851.5	86.9	417	11	O88691
3	1788	83.9	418	11	O802A3
4	1784	83.7	362	4	Q13236
5	537	25.2	448	13	O42453
6	456.5	21.4	491	4	Q8N5U7
7	453	21.3	471	11	Q80X76
8	441.5	20.7	420	11	Q60552
9	429.5	20.2	415	6	Q9GMA6
10	421	19.8	418	11	Q8VCH3
11	420	19.7	418	11	Q91X80
12	418	19.6	418	11	Q03734
13	418	19.6	423	11	P97569
14	417	19.6	406	11	Q64118
15	416.5	19.5	418	11	Q91WP6
16	416.5	19.5	418	11	Q62258

17	416	19.5	418	11	Q91W80
18	413	19.4	412	11	Q63556
19	411.5	19.3	396	6	O00394
20	406.5	19.1	411	6	Q9TTE1
21	403	18.9	413	6	Q07298
22	402	18.9	413	11	Q7TME5
23	400	18.8	375	11	Q8K3Y1
24	400	18.8	418	11	Q62257
25	399	18.7	413	11	Q9CQ32
26	396	18.6	413	6	Q28665
27	395.5	18.6	423	11	Q63969
28	395.5	18.6	423	4	Q8N177
29	393.5	18.5	432	13	Q7SYX0
30	392.5	18.4	500	4	Q9AEP0
31	392	18.4	405	4	Q722Q9
32	391.5	18.4	421	6	O46519
33	390.5	18.3	413	11	O54761
34	390.5	18.3	440	4	Q86U17
35	387	18.2	456	6	O62663
36	385.5	18.1	407	4	Q9UNU9
37	384	18.0	413	6	Q28666
38	383.5	18.0	413	11	O54762
39	382	17.9	379	11	Q9D154
40	381.5	17.9	413	11	Q91XB8
41	381.5	17.9	413	11	Q8VC20
42	381.5	17.9	422	11	Q80YB8
43	381.5	17.9	425	11	Q80ZHS
44	381.5	17.9	436	11	Q8ZV6
45	381	17.9	418	11	Q9D7D2

ALIGNMENTS

RESULT 1
O70629
ID O70629 PRELIMINARY; PRT; 417 AA.
AC O70629;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pigment epithelium-derived factor (Serine (or cysteine) proteinase inhibitor, clade F (Alpha-2 antiplasmin, pigment epithelium derived factor). member 1)).
DE factor). member 1)).
GN SERPINF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Singh V.K., Chader G.J., Rodriguez I.R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF017055; AAC05733.1; JOINED.
DR EMBL; AF017051; AAC05733.1; JOINED.
DR EMBL; AF017052; AAC05733.1; JOINED.
DR EMBL; AF017053; AAC05733.1; JOINED.
DR EMBL; AF017054; AAC05733.1; JOINED.
DR EMBL; AF017057; AAC05731.1; JOINED.
DR EMBL; BC019852; AAH19852.1; JOINED.
DR HSSP; P36955; 1IMV.
DR MGD; MGI:108080; Serpinf1.
DR CO; CO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.

Protease inhibitor; Serine protease inhibitor; Serpin.
KW PROTEASE INHIBITOR; SERINE PROTEASE INHIBITOR; SERPIN.
SQ SEQUENCE 417 AA; 46234 MW; ECD360FE6AA74D25 CRC64;

Query Match	87.1%;	Score 1856.5;	DB 11;	Length 417;
Best Local Similarity	86.5%;	Pred. No. 1.6e-136;		
Matches 360;	Conservative	34;	Mismatches 19;	Indels 3;
			Gaps 2;	

QY	1	MOA	VLLLCIGALLGHSQCN--PASPPBEGSPDPDSTGALVEBEDPPFKVPVKNKLAANA59	59
Db	1	MOA	VLLLTWTGALLGHSQNVPS--SEGSPVPDSTGEPVEBEDPPFKVPVKNKLAANA58	58
QY	60	NGY	DLRVRSMSPTTNVLLSPUSVATALSALSGAEQRTESIHRALYYDLTISPDTH119	119
Db	59	NGY	DLRYRSASPTGNVLLSPUSVATALSALSGAEHRTESVIHRALYYDLTTPDTH118	118
QY	120	GTY	KELLDTVTAPQKNLASARIYFEKKLIRKSSFAPLEKSYGTRPRVLITGNPRLDQE179	179
Db	119	STY	KELLASVTAPEKNLASARIYFERKLIRKVSFVAPLEKSYGTRPRIITGNPRVDQE178	178
QY	180	INN	VQAOQMKGLARSTKEIDETSILLGVAFKQGWTKFDSRKTSLDFVLDSERTV239	239
Db	179	INN	VQAOQMKGIARSTREMPSSALLLGVAYFKQGWTKFDSRKTTLQDFLDSERTV238	238
QY	240	RYPM	SDPKAVLYRGLDSDLCKTAQLPLTGSMSIIRFELPKYTONLTLEESLTSEFTH299	299
Db	239	RYPM	SDPKAILRYGLDSDLNCKTAQLPLTGSMSIIRFELPTVTONLTLEESLTSEFTH298	298
QY	300	DIDR	EKLTVQAVLTPVKLKSVEGEVTKSLQEMKLSQSLFSDPSFKITGPKILTOVEHR359	359
Db	299	DIDR	EKLTKTQAVLTPVKLKSPEGBLTKSLQDMKLSLFSFSDPSFKITGPKVILTOVEHR358	358
QY	360	AGF	EMNEDGAGTTPSGLOPAHLTPFLDYHLNQPPIFVLRTDTPGALLFTGKILDP415	415
Db	359	AAFE	NEEGAGSSPGIOPVRLTPEFLDYHLNQPPIFVLRTDTPGALLFTGKILDP414	414

RESULT 2

ID	088691.
ID	C88691 PRELIMINARY; PRT: 417 AA.
AC	C88691;
DT	01-NOV-1998 (TrEMBLrel. 08, Created)
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Capsin.
DI	SERPINF1.
GN	Mus musculus (Mouse).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC	NCBI_Taxid=10090;
[1]	SEQUENCE FROM N.A.
RN	STRAIN=BALB/c; TISSUE=Liver;
RC	MEDLINE=98279032; PubMed=96141424;
RX	Kozaki K., Miyaishi O., Koiwai O., Yasui Y., Kashiwai A.,
RA	Nishikawa Y., Shimizu S., Saga S.,
RT	"Isolation, purification and characterization of a collagen-associated
RT	serpin, capsin, produced by murine colon adenocarcinoma cells.";
RL	J. Biol. Chem. 273:15125-15130(1998).
CC	-I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR	EMBL: D87915; BAA31978.1; -.
DR	HSSP: P36945; 11MW.
DR	GMD: MGI:108080; Serpinf1.
DR	GO: GO:0004867; F:serine protease inhibitor activity; IEA.
DR	InterPro: IPR000215; Serpin.
DR	Pfam: PF00079; serpin; 1.
DR	SMART: SM00093; SERPIN; 1.
DR	PROSITE: PSQ0284; SERPIN; 1.
SW	Protease inhibitor; Serine protease inhibitor; Serpin.
SC	SEQUENCE 417 AA; 46220 MW; ADD224FA2BA51A00 CRC64;

Query Match	Score	DB 11	Length
Best Local Similarity	86.9%	151.5	417
Matches	359		
Conservative	34		
Mismatches	20		
Indels	3		
Gaps	2		

QY	1	MOALVLLICTGALLGHSSCON--FASPPERGSDPDSTGALVEEEDPFFKVPVWKLAAAVS	59
Db	1	MOALVLLTWTGALLGHSSQNVPS--SGSPVPDSTGPEVEEEDPFFKVPVWKLAAAVS	58
QY	60	NFGYDLVRVRSSMPTTNVLLSPLSVATALSALSLGAEQRTESIIRHALYYDLISSPDH	119
Db	59	NFGYDLYELRASSAPTGNVLLSPLSVATALSALSLGAEHRTESVIRHALYYDLITNPDIH	118
QY	120	GTYYKELDTVTAPQNKUKSARIVFEKKRIKSFVAPELXSYGTRPRVLTGNRPRLDQE	179
Db	119	STYKELLASVTAPKPNLNSASRIIVFERKURKSSFVAPELXSYGTRPRILTGNRPVLDQE	178
QY	180	INNVVQAQMKGLARSTKEIPDISIILLGLCVAHFKQWTKFDSRKTSLIEDFYLDDEETV	239
Db	179	INNVVQAQMKGKIARSTREWPALSILLGLGVAYFKQWTKFDSRKTLLQDFHLDERTV	238
QY	240	RVPMSDPAVRLYGLSDLSCKIAQLPTGVSIIFFLPKVTQNTQLLIBESLTSEFIH	299
Db	239	RVPMSDPKALIRYGLSDLNCKIAQLPTGSMIIFFLPVTQNTQLTWIEESLTSEFIH	298
QY	300	DIDRELKTQAVLTVPKLLSYGEVTKSLQEMKLSLSDPSDFSKITGPKIKLTQVEHR	359
Db	299	DIDRELKTIQAVLTVPKLLSFGEELTKSLQDNKLSLSDPSDFSKITGPKVLTQVEHR	358
QY	360	AGFENWEDGACTTSPGLQPAHITFFLDYHLNPOFFIVLRDRTDTGALLFIGKILDP	415
Db	359	AAFEWNEEGAGGSDSPGLQPVRLTFFLDYHLNPFVLVRDRTDTGALLFIGRILDP	414
RESULT 3			
Q80ZA3			
ID	Q80ZA3	PRELIMINARY;	PRT; 418 AA.
AC	Q80ZA3;		
DT	01-JUN-2003 (TreeBLrel. 24, Created)		
DT	01-JUN-2003 (TreeBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TreeBLrel. 25, Last annotation update)		
DE	Alpha-2 antipiasmin.		
DN	DMRS91.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
QC	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague Dawley; TISSUE=Kidney;		
RL	Yang J.L., Yang Y.S., Li G., Luo M.		
RA	Submitted (JAN-2003), to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY215665; AAC60104.1; -.		
DR	GO; GO:0004867; F:serine protease inhibitor activity; IEA.		
DR	InterPro; IPR000215; Serpin.		
DR	Pfam; PF000079; serpin; 1.		
DR	SMART; SM00093; serpin; 1.		
DR	PROSITE; PS00284; SERPIN; 1.		
SO	SEQUENCE 418 AA; 46465 MW; 5C7CAFB5D5199880F CRC64;		

Query Match	83.9%	Score	1788;	DB	11;	Length	418;
Best Local Similarity	83.2%;	Pred. No.	3.5e-131;				
Matches	347;	Conservative	37;	Mismatches	29;	Indels	4; Gaps
Qy	1	MOALVLLICIGALLCHSCQN-PASPEEGSPDPDSTG-ALVBEEDPFFKVPVNKLAAAV	58				
		: :					
Db	1	MTLVLLWTGALLGHSSQNVPDS--SQDSPADSTGERVVEEDPFFKAPVNKLAAAV	58				
		: :					
Qy	59	SNFGYDLVRVRSSMSPPTNVLLSPLSVATLALSLSGAERTESIHRALYLDLTSSPDI	118				
		: :					
Db	59	SNFGYDLVRLRSGAVSTGNILLSPLSVATLALSLSGAERTESIVHRALYLDLTNNPDI	118				
		: :					
Qy	119	HGTGYKELDTVTAPQNLKSARIVFPEKKLIKSSFPVPLEKSYGRPRVLTCGNPRLDIQ	178				
		: :					
Db	119	HTYIKELLASVTAPENKFASRIIVFERKLRVSSFPVPLEKSYGTFPRILTCGNPRLDIQ	178				
		: :					
Qy	179	EINNVMVQAMKGKLARSKEIPDEISILLGVAFHKQGWTKFDPSRKTSLSDFYLDEERT	238				

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Db 179 EINNVOAQMGKARSTREMPSSALSILLGVAVFGQWATKFSRKTTLQDFHLEDDRT 238
Qy 239 VRVPMSPDKAVRLGYGLSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFI 298
Db 239 VRVPMSPDKAILRYGLSDLSCKIAQLPLTGSMSIIFFLPLVTQNLTLIEESLTSEFV 298
Qy 299 HDIRELKTQAVLTVPKLSYGEVTKSLQEMKLSLDFSDPFSKITGPKLQVH 358
Db 299 HDIRELKTQAVLTVPKLSYGEVTKSLQEMKLSLDFSDPFSKITGPKLQVH 358
Qy 359 RAGFEWNEGAGTTPSQLOPAHLTFPLDYHLNPPFVLRDITDTGALLFIGKILDP 415
Db 359 RAGFEWNEGAGTSSNDLPQVRLTFPLDYHLNPPFVLRDITDTGALLFIGKILDP 415

RESULT 4
Q13236 PRELIMINARY; PRT; 362 AA.
AC Q13236;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pigment epithelium-derived factor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tombran-Tink, J, Mazuruk, K, Rodriguez I., Kouri R.E., Chung D.,
RA Linker T., Chader G.J.;
RT "Cloning and molecular characterization of the human gene for the
RT neurotrophic serpin PEDF: conservation, polymorphism and hereditary
RT studies."
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; U29953; AAA84914.1; -.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR HSP; P36955; 11MV.
DR InterPro: IPR00215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR SWART; SM00093; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 362 AA; 40071 MW; 650E4C63767B54DD CRC64;

Query Match 83.78; Score 1784; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.8e-131; Indels 0; Gaps 0;
Matches 358; Conservative 0; Mismatches 0;

Qy 1 MQALVLLCIGALLGHSSCCNPASPPPEGSPDSTGALVEEDPFFKVPVKNKLAASVN 60
Db 1 MQALVLLCIGALLGHSSCCNPASPPPEGSPDSTGALVEEDPFFKVPVKNKLAASVN 60
Qy 61 FGDLVYRVSMSPTTNVLLSPVATLSALSGAEQRTESIHRALYDLISSPDHIG 120
Db 61 FGDLVYRVSMSPTTNVLLSPVATLSALSGAEQRTESIHRALYDLISSPDHIG 120
Qy 121 TYKELLDTVTAQPKNLKASRIVFEKKLRKSSFPVAPLEKSYGTRPRVLTGNPRLDLQEI 180
Db 121 TYKELLDTVTAQPKNLKASRIVFEKKLRKSSFPVAPLEKSYGTRPRVLTGNPRLDLQEI 180
Qy 181 NNWVQAQMGKARSTKEIPEISILLGVAVFGQWATKFSRKTSLDFYLDERTVR 240
Db 181 NNWVQAQMGKARSTKEIPEISILLGVAVFGQWATKFSRKTSLDFYLDERTVR 240
Qy 241 VPMMSDPKAVRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFIH 300
Db 241 VPMMSDPKAVRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFIH 300
Qy 301 IDRELKTQAVLTVPKLSYGEVTKSLQEMKLSLDFSDPFSKITGPKIKLTQ 355
Db 301 IDRELKTQAVLTVPKLSYGEVTKSLQEMKLSLDFSDPFSKITGPKIKLTQ 355
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RESULT 5
Q42453 PRELIMINARY; PRT; 448 AA.
AC Q42453;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Serpin precursor.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzoniformes; Petromyzontidae; Petromyzon.
OC NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larval liver;
RA Robson P., Li F., Youson J.H., Keeley F.W.;
RT "Identification and characterization of a serpin with differential
RT expression during the life cycle of the sea lamprey,"
RL Comp. Biochem. Physiol. B, Comp. Biochem. 120:253-263 (1998).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF009964; AAC63406.1; -.
DR HSP; P01012; IOVA.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro: IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 448
SQ SEQUENCE 448 AA; 49044 MW; 5F925AC1B45FDFE9 CRC64;

Query Match 25.2%; Score 537; DB 13; Length 448;
Best Local Similarity 29.6%; Pred. No. 2e-33;
Matches 123; Conservative 91; Mismatches 183; Indels 18; Gaps 6;

Qy 4 LVLLCIGALLGHSSCCNPASPPPEGSPDSTGALVEEDPFFKVPVKNKLAASVNFQY 63
Db 12 LVTLISLG-FADHGHTEFGAPPV-----SATAI-----SPFV---VSRLAGSQDGFQ 56
Qy 64 DLYRVSMSPTTNVLLSPVATLSALSGAEQRTESIHRALYDLISSPDHIGTYK 123
Db 57 QFFHKLGEASPCQNVLFSPPLTSAALMMLLAGSGDKTQLTNALRLQFLRDPNPAQSFQ 116
Qy 124 ELLDVTVAQPKNLKASRIVFEKKLRKSSFPVAPLEKSYGTRPRVLTGNPRLDLQEI 183
Db 117 ALVSKLHGRDSTNTAARIFTAKHATIKQQLDAVEKYKAKPQKLIGNMKEDVALINKW 176
Qy 184 VQAQMGKARSTKEIPEISILLGVAVFGQWATKFSRKTSLDFYLDERTVRVPM 243
Db 177 VAEKTEGHIIDPVKELPEELQLFIVSAIFFKGMKLPQVESTSPRPHLSPSNETQVPT 236
Qy 244 MSDPKAVRYGLSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFIH 303
Db 237 MFASGPYIKKGHPSPVTVAKIQQNTSLLLFFVDAVSTNLSALESSLQVLTTLVE 296
Qy 304 ELKTVQAV-LTVPKLKLSEGEVTKSLQEMKLSLDFSDPFSKITGPKIKLTQVSHRAGF 362
Db 297 ETLVQKKTDLVPLISLDVESNIEQKLDIGLDLFTKPTDLSKISDILPVSKVHIRATM 356
Qy 363 ENNEGAGTTPSQLOPAHLTFPLDYHL--NOPFFVLRDITDTGALLFIGKILDP 415
Db 357 TLNEEGVKATAATGIMISLVQSHSEELKVDPRPFVLRDITDETGALEFVGRVTS 411

RESULT 6
Q8N507 PRELIMINARY; PRT; 491 AA.
AC Q8N507;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Kidney;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: AAH31592; AAH31592.1; -.
DR EMBL; BC031592; AAH31592.1; -.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Hypothetical protein; Protease inhibitor; Serine protease inhibitor;
KW Serpin.
SQ SEQUENCE 491 AA; 54593 MW; 9CCF5B1D21C6EE03 CRC64;

Query Match 21.48; Score 456.5; DB 4; Length 491;
Best Local Similarity 28.44; Pred. No. 4.5e-27;
Matches 127; Conservative 86; Mismatches 181; Indels 53; Gaps 11;

QY 5 VLLICIGALLGHSCQNPAS-----PPEE-----GSPDPSTGAL--- 39
DB 7 LLVLSWCLQPCSVFSPVSAEPLRGLTSGFNQGVSPLETLKLGNEPGQQTALKSP 66
QY 40 --VEEEDPFKVP--VNKLAAVSNFGYDLYRVRSMSPTNVLSPLSVATALSLSLG 95
DB 67 PGVCSRDP---TPEQTHRLARMAFAFTADLSVAQTSTCPNLSPLSVALSLSHLG 123
QY 96 AE-----RTESIIRALYDLSIPDHGTYKSLIDTDTVAPOXNLKSASRIVEKRLIK 151
DB 124 AQNHTLQRLQVHLAG-----SGPCLPHLSRLQCDLGPAGRL--AARMYLQKFPPIK 175
QY 152 SSFVAPLEKSYGTRPRVLTGNPRLDQEIINNVOAQMKGKLARSTKEIDPESILLGVA 211
DB 176 EDFLEQSEQLFGAKFVSLTKQEDDLANINQWKEATEGKIQFSLGSLPEDTVLLNLAI 235
QY 212 HFKGQWTKDSRSTSLDFYLBERTVVRPMKSDPKAVLYRGLDLSCKIAQLPLTGS 271
DB 236 HFQGFWRNKDPSLTQRDSFHLDEQFTVPMKQARTYPLRWFLLEQPEIQVAHFFPKN 295
QY 272 MSIIFFPLKVTQNTLIEESLTSEFIHD---IDRELKTVOAVLTVPKLSYEGEVTKS 328
DB 296 MSFVLVPTHFEMVNSQVLANLSWDLTHPLVWERPTK-----VRLPKLYLKHQMDLVAT 350
QY 329 LOEMKLSLSDSPDFSKITGPKIKLTOVEHRAGFENEDGAGTTPSPGLQPAHLTFPLDY 388
DB 351 LSQGLQELFQAPLRGIGSQSLVSGVGHQSTLEUSEVGEVAAAATSIAMSRNLS-SF 409
QY 389 HLNQPFIFVLRTDTGALLFGIKLDP 415
DB 410 SVNRPFLFFIEDTGLPLFVGSRNP 436

RESULT 7
ID Q80X76 PRELIMINARY; PRT; 471 AA.
AC Q80X76;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LOC238393 protein (fragment).
GN LOC238393.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Heigh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Rada S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaby S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gumarane P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywinski M.I.; Skalska U.; Smallos D.B.; Scherch A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049975; AAH49975.1; -.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
FT NON TER 1
SQ SEQUENCE 471 AA; 52756 MW; 482DB301DB9D8BEA CRC64;

Query Match 21.34; Score 453; DB 11; Length 471;
Best Local Similarity 30.14; Pred. No. 7.9e-27;
Matches 123; Conservative 81; Mismatches 184; Indels 20; Gaps 10;

QY 24 SPPEEGSDP--DSTGALVEEEDFFKVPVNKLAAVSNFGYDLYRVRSMSPTNVLIS 81
DB 31 SPVAFGCPDVLGRNTAVREVENITSDVSLTASSNTDFAFSLYKELVKNPDENVVFS 90
QY 82 PLSVATALSALSGAQRTESIIRALYDLS--PDHCTYKELDTVTAP--OKNLX 137
DB 91 PFSICTALTLSLGAKNLTKEILEGLKFNLTETPEPDHGGFRYLLDLSQPNQVQIS 150
QY 138 SASRIVFEKLRIRKSSFVAPLEKSYGTRPRVLTGNPRLDQE---INNVOAQMKGKLAR 194
DB 151 TGSALFIEKHQILAEFEKARALY--QAFAFTADFOQPLEATKINDYVSNQTOGIKE 208
QY 195 STKEIPDEISILLGVAFHFGQWTKFDSRSTSLDFYLBERTVVRPMKSDPKAVLYRG 254
DB 209 LISDLKRTLMVLVNIYIFKGMWEPDPDDTCKSEFYLDENRSKVPKMKINLTTPTF 268
QY 255 LDSLSCKIAQLPLTGSMSIIFPLKVTQNTLIEESLTSEFIHDIDRELK-TVQAVLT 313
DB 269 RDELSCTVVELKVTGNASAFILPDQ--GKQQQVEASLQPETLRNWKDSLKPLIDELC 326
QY 314 VPKLSYEGEVTKSLQEMKLSQSLFDS--PDFSKITG-KPKILTOVEHRAGFENEDGAGT 371
DB 327 LPKFSISTDYSLEHILPELGRLEFSTQADLSAITGTKDLRTSQVHVHAKVLDVAETGEA 386
QY 372 TSPSGLOPAH---LTPPLDYHLNQPFIPLVLRDGTGALLFGIKLDP 415
DB 387 AAGTGYQLQCCQGVIVSMKIYFDRPFLMIISDINTHIALFMKVTP 434

RESULT 8
Q60552
ID Q60552 PRELIMINARY; PRT; 420 AA.
```

AC Q60552;
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pregnancy protein 60 kDa precursor.
GN HPP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Waterhouse; TISSUE=Liver;
EA Park C.G.;
RT "Cloning and sequencing of a new pregnancy marker protein from hamster
RT liver";
RL Thesis (1992), Biological Sciences, The Wichita State University.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; M96650; AAA37078.1; -.
DR HSSP; P01011; 1A54.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 420 PREGNANCY PROTEIN 60 KDA.
FT SEQUENCE 420 AA; 47490 MW; 3B9859D19A034EFA CRC64;
Query Match 20.7%; Score 441.5; DB 11; Length 420;
Best Local Similarity 28.0%; Pred. No. 5.3e-26;
Matches 123; Conservative 90; Mismatches 175; Indels 51; Gaps 11;
QY 4 LVLLCTGALLGSSQCPASPPGSPDPSTGALVEEDPFKVPVKNKLAASVNFY 63
Db 5 VAFILLVAAPCPALVC-----QDGLTKETT--VOEQNNETKVDLSLTASINTDFAF 56
QY 64 DLVVRSSMPTTNVLLSPLSVATLSALSLGAEQRTESIHRALYYDLTSSP--DIHGT 121
Db 57 SLYKQLAKPKDKVIFSPFSISFALAFSLGASSNTLEILGLKFNLTETEDAIHRG 116
QY 122 YKELLDTVTAP--QKNLKSASRIVFEKKLRKISFVAPLEKSYGTGTRPVLTGNPRLDQ 179
Db 117 FGHLLRLMSQPGDQVQVSTSSAMFEVKRLQLIAEFKKKARALYCAEA-----SSTD 170
QY 180 -----INNVQQAQMGKGLARSTKEIPDEISILLGVAFHFGQVTKFDSRKTSLDFY 232
Db 171 PHEAKKLINDYVSKTTHGKIKELMSDDDDQTSWVLVNIYFKGKWKAPFPDFYESDFY 230
QY 233 LDEERTVVRPMSPKAVLRGLDSDLSCKIAQLPLTGSMSTIFFLPLK-----V 282
Db 231 LDNKRKVPKMKHKDLTTPYFRDEELSSYVEMRYGNVSAMFILPKGRMQQLLESSLQ 290
QY 283 TQNTLLEESLTSFFIHIDRELKTVQAVLTVPKLSYGEVTKSLQEMKLSLQSDS-P 341
Db 291 PETLRWKDSLRPMIHE-----LYVPKFSISTDYSMEGLSQGIKEVFSSQA 339
QY 342 DFSKITG-KPKLTQVEHRAAGFENWEDGAGTTPSPGLQ---PAHLTPFLDYHLNQPFIFV 397
Db 340 DLSGITGDKLRSVKVVKHKAVDLGVETGTEAAATGLRWGSAIINPLRLRNKPKFLMI 399
QY 398 LRDTDTGALLPFGIKLDP 416
Db 400 IYNTNTQTPLFMKVTNPK 418
RESULT 9
Q9GMA6 PRELIMINARY; PRT; 415 AA.
AC Q9GMA6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
GN AACT2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9923;
RN [1]
RP SEQUENCE FROM N.A.
RC Stratil A.; Peelman L.; Mattheeuws M.;
RT "The porcine alpha-1-antichymotrypsin 2 (AACT2) gene: nucleotide
RT sequence, genomic organization and polymorphism";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AJ297654; CAC05490.1; -.
DR HSSP; P01011; 1A54.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 415 ALPHA-1-ANTICHYMOTRYPIN 2.
FT VARIANT 399 399 I -> V.
FT VARIANT 401 401 K -> N.
FT SEQUENCE 415 AA; 46645 MW; EF29767E63D59060 CRC64;
Query Match 20.2%; Score 429.5; DB 6; Length 415;
Best Local Similarity 28.3%; Pred. No. 4.5e-25;
Matches 121; Conservative 87; Mismatches 188; Indels 31; Gaps 11;
QY 4 LVLLCTGALLGSSQCPASPPGSPDPSTGALVEEDPFKVPVKNKLAASVNFY 61
Db 5 LALGLLVAGLCRVEHC-----VPADDPASKIVTLKQIKLPAHNTAVVSSNTDF 54
QY 62 GYDLVVRSSMPTTNVLLSPLSVATLSALSLGAEQRTESIHRALYYDLTSSP--DIH 119
Db 55 AFSLYKQLALTNPHENVIFSPLSVSMALAFSLGARGPTLTLEGLKFNLTKEABIH 114
QY 120 GYKELLDTVTAPQK--NLKSASRIVFEKKLRKISFVAPLEKSY-----GTRPVLTGN 172
Db 115 QCFQHLSTLDRSSNLLQLRLGNAMFIDEQLELDFKVDQDAHELYHSEAFPTNFQDL 174
QY 173 PLDLQELNNWQAQMGKGLARSTKEIPDEISILLGVAFHFGQVTKFDSRKTSLDFY 232
Db 175 RL-----INDYVKNTEGKIVDLFKKLDPLTKVILVNIYFKAKWKTFPNLTT 230
QY 233 LDEERTVVRPMSPKAVLRGLDSDLSCKIAQLPLTGSMSTIFFLPLKVTQNTL 292
Db 231 VSKNRTVVRPMGIRALTVPYFRDEELACTVVELFPTSNDLSALFLP--DDGRMAA 288
QY 293 LTSEFIHIDRELKTVQAV-LTVPKLSYGEVTKSLQEMKLSLQSDS-P 349
Db 289 LPETLRWKDQLQRPWIVELYLPKFSISSDVRHLHEILPQGIIEIFGNANLSIT 348
QY 350 PIKLTQVEHRAAGFENWEDGAGTTPSPGLQ-PAHLTPFLDYHLNQPFIFVLRD 408
Db 349 PLKVSQVHSAVLDVNEEGTEAAATGIDINVRSLERIALHFNRPFLFIISKDIQ 408
QY 409 ICKILDP 415
Db 409 LGKVTKP 415
RESULT 10
Q8VCH3 PRELIMINARY; PRT; 418 AA.
AC Q8VCH3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Serine protease inhibitor 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC019802; AAH19802.1; -.
DR HSP; P01009; IOLP.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 418 AA; 46851 MW; DF5D6C0362F3A291 CRC64;

Query Match 19.8%; Score 421; DB 11; Length 418;
Best Local Similarity 30.9%; Pred. No. 2.1e-24;
Matches 118; Conservative 80; Mismatches 154; Indels 30; Gaps 12;

QY 54 LAAAVSFGDYLYVRSSMPTTNVLLSPLSVATLSALSALGAEQRTESIIRHLYYDLI 113
DB 48 LASVNTDFAFSLYKALKKPNPTNIVFSPUSISAAALVSLGAKGTMBEILGLKFNLT 107
QY 114 SSP--DIHGTYKELLDTVTAP--QKNLKSASRIVFEKRIKSSFVAPLEKSYGTRPRVL 169
DB 108 ETPEADIHQGFGLNLSQSPEDQDQINIGNAMFIEKDQLAEF---HEK---TRALYQ 161
QY 170 TGNPRLDQ-----INNVOAQMKGLARSTKIPDEISILLGVAFHKGOWTKFD 222
DB 162 TEAFTADFOQTEAKNLINDYVSNQGTGMKELISELDELTMLVNLVNYIFKGNKWSFD 221
QY 223 SRKTSLEDFYLDERTVVRPMSPDKAVLYRGDLSCKIAQLPLTSGMSIIFFLPKV 282
DB 222 PQDTFSEFYLDEKRSVKVPMKMKLLTRHFRDEELSCVLELKYTGNASALLILPDQ- 280
QY 283 TQNLTLIESLTSEFHDIDRELKTQV-AVLTVPKLKSVEGEVTKS-LOEMKLSLF-D 339
DB 281 -GRMQQVEASLPQETLRKWRKTLFPFSQIEELNLPKFSIASNYRLESDVLPENGKEVFTE 339
QY 340 SPDSKIT-GKPIKLTQVEHRAQFENEDG---AGTTPSPGLQPAHLTPPLDYHLNQPF 394
DB 340 QADLSGITETKLSVSQVHKAVLDVAETGTEAAATGVIGGIRKAILP---GVHFNRRPF 396
QY 395 IFVLRDITDGTALLFIGKILDP 416
DB 397 LFVIYHTSAQSILFMKVNPNK 418

RESULT 11
Q91X80 PRELIMINARY; PRT; 418 AA.
AC Q91X80
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Serine protease inhibitor 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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DR EMBL; BC011217; AAH11217.1; -.
DR HSP; P01009; IOLP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 418 AA; 46866 MW; DF5D6C0362F5C2F7 CRC64;

Query Match 19.7%; Score 420; DB 11; Length 418;
Best Local Similarity 30.9%; Pred. No. 2.5e-24;
Matches 118; Conservative 80; Mismatches 154; Indels 30; Gaps 12;

QY 54 LAAAVSFGDYLYVRSSMPTTNVLLSPLSVATLSALSALGAEQRTESIIRHLYYDLI 113
DB 48 LASVNTDFAFSLYKALKKPNPTNIVFSPUSISAAALVSLGAKGTMBEILGLKFNLT 107
QY 114 SSP--DIHGTYKELLDTVTAP--QKNLKSASRIVFEKRIKSSFVAPLEKSYGTRPRVL 169
DB 108 ETPEADIHQGFGLNLSQSPEDQDQINIGNAMFIEKDQLAEF---HEK---TRALYQ 161
QY 170 TGNPRLDQ-----INNVOAQMKGLARSTKIPDEISILLGVAFHKGOWTKFD 222
DB 162 TEAFTADFOQTEAKNLINDYVSNQGTGMKELISELDELTMLVNLVNYIFKGNKWSFD 221
QY 223 SRKTSLEDFYLDERTVVRPMSPDKAVLYRGDLSCKIAQLPLTSGMSIIFFLPKV 282
DB 222 PQDTFSEFYLDEKRSVKVPMKMKLLTRHFRDEELSCVLELKYTGNASALLILPDQ- 280
QY 283 TQNLTLIESLTSEFHDIDRELKTQV-AVLTVPKLKSVEGEVTKS-LOEMKLSLF-D 339
DB 281 -GRMQQVEASLPQETLRKWRKTLFPFSQIEELNLPKFSIASNYRLESDVLPENGKEVFTE 339
QY 340 SPDSKIT-GKPIKLTQVEHRAQFENEDG---AGTTPSPGLQPAHLTPPLDYHLNQPF 394
DB 340 QADLSGITETKLSVSQVHKAVLDVAETGTEAAATGVIGGIRKAILP---AVHFNRRPF 396
QY 395 IFVLRDITDGTALLFIGKILDP 416
DB 397 LFVIYHTSAQSILFMKVNPNK 418

RESULT 12
Q03734 PRELIMINARY; PRT; 418 AA.
AC Q03734
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Contrapsin related protein (Similar to serine protease inhibitor-2 related sequence 1) (Serine (or cysteine) proteinase inhibitor, clade A, member 3M).
OS SERPINA3M OR SP12-RS1 OR CMC7.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Ohkubo K., Ogata S., Misumi Y., Takami N., Sinohara H., Ikahata Y.;
RT "Cloning, structure, and expression of mouse contrapsin and its related protein.";
RL Biochem. J. 0:0-0(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR ENBL; X53148; CAA38949.1; -.
DR ENBL; BC011158; AAH11158.1; -.
DR ENBL; BC053337; AAH53337.1; -.
DR PIR; S23675; S23675.
DR HSP; P01011; 2ACH.
DR MGD; MGI:98378; Serpina3m.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 418 AA; 47004 MW; 32D957F693B69B79 CRC64;

Query Match 19.6%; Score 418; DB 11; Length 418;
Best Local Similarity 28.8%; Pred. No. 3.6e-24;
Matches 119; Conservative 75; Mismatches 165; Indels 54; Gaps 11;

QY 27 EGSPDPSICALVEEDPEKYPVNKLAASVNFYDLYVRSSMPTNVLVLSVA 86
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 87 TALSALSLGAEQRTESIIRALYYDL--ISSPDHGTYSKELLDTVTAP--QKNLKSASRI 142
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 143 VFEKLRKISFVAPLEKSYGTGPRVLTGNPRDLQD-----INNVOAQMKGLKARS 195
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 140 FIEKDLQILAEFEKARALYQTEFT-----ADFQKTEAKNLINDYVSNQTQGMKEL 193
QY 196 TKETPDSEISILLGVAFKQGWTKPDSRKTSLEDFDLDEERTVRYPMMSDPKAVLRYGL 255
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 194 ISELDTDTLMVLNVNIYFKGKWKISFPDQTFSEFVLEKRSVKVPMKMKELTTRHFR 253
QY 256 DSDLCKIAQLPDTGNSMIIFFPLKVTQNLTLIESLTSFTHIDRELKTVQ-AVLTV 314
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 254 DEELSCSVLELKYTGASALFILPDQ--GRMQQVEASLQPETLRKWKWSLKTRKIGELYL 311
QY 315 PKLKLISYEGEVTSLQMKLQSLFD-SPDFSKITG-KPIKLTOVEHRAGFENNEDGAGIT 372
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 312 PKFSISTDYNLKKDILPELGRKIFSGKQADLSGITGKLSVQVHKAVLDVAETGEAA 371
QY 373 PSPG-----LQPAHLTFPLDYHLNPPFIFVLRTDTGTGALLFICKILDPR 416
: |||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 372 AATGFIQFGRSRRRLQMTVTQVF-----NRPFLMWISHTGVQTTLFMAKVTNPK 418

RESULT 13
P97569
ID P97569 PRELIMINARY; PRT; 423 AA.
AC P97569;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Kallistatin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116; [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Chai K.X., Ni A., Chen V.C., Lindpaintner K., Rubattu S., Chao J.,
RA Chao L.;
RT "Molecular cloning and characterization of the rat kallistatin gene.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR ENBL; U51017; AAB39509.1; -.
DR HSP; P01011; 1AS4.
DR GO; GO:0004867; R:serine protease inhibitor activity; IEA.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 423 AA; 48021 MW; 133456709BDB2FE9 CRC64;

Query Match 19.6%; Score 418; DB 11; Length 423;
Best Local Similarity 28.3%; Pred. No. 3.6e-24;
Matches 122; Conservative 94; Mismatches 179; Indels 36; Gaps 14;

QY 5 VLLLCIGAL-IGHSSCONPAPPEGSDPDSTGALVEEDPEFFKYPVNKLAASVNFY 63
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 64 DLYVRSSMPTNVLVLSPLSVATLSALSGAEQRTESIIRALYYDL--ISSPDHGT 121
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 58 RLYHLIASQNSEKNIFSFPLSGTSLTSLTSGAGDQALLEGGLNLTSLPEIHG 117
QY 122 KYELDTVTAP--QKNLKSASRIPEKLRJSSVAPLEKSYGTGPRVLTGNPR--LD 176
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 FSLQHTTARPTETPOISVSGALILSLQNLILSEFVSAIETSYNS--KVLHANFRDKAA 175
QY 177 LQEIINNVOAQMKGLKARSTKEIPDEISILLGVAFKQGWTKPDSRKTSLEDFYLD 236
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 176 VOLINNVYKQNTQGIKNLVSDLSDPDKVNLVNIYFFQGLWKPKPPFSRVSTSD 235
QY 237 RTVRYPMMSDPKAVLRYGLDSDLCKIAQLPDTGNSMIIFFPLKVTQNLTLIESL 296
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 236 TVVKIPMKLQDKEHDHWHLEDRVPCTVLRMDYRGDAVFAFFILPDQGN--EVEQV 293
QY 297 FTHIDRELKT-----VQAVLTVPKLSYEGEVTSLQMKLQSLF-DSPDFSKITG-K 350
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 294 MLLRWKRLQLNRRFFYRKLIQLPKFSISNSYELDEILPDGLQDFTFNANFSN 353
QY 351 IKLTOVEHRAGFENNEDGAGITPSPGLQPAHLTF-----PLDYHL--NOPPF 404
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 354 LYLKVFVFKTKVLDNVNEVGTAKAAATG---SPATFSAQPKKRYLIFNRPFLV 410
QY 405 ALLFTICKILD 415
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 411 DILFVGKVNVP 421
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
Q64118 PRELIMINARY; PRT; 406 AA.
ID Q64118

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AC Q64118;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha-1-antitrypsinase.
 DE Meriones unguliculatus (Mongolian jird) (Mongolian gerbil).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC Meriones.
 OC NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9515526; PubMed=7852275;
 RX Goto K., Suzuki Y., Yoshida K., Yamamoto K., Sinchara H.;
 RT "Plasma, alpha-1-antitrypsinase from the Mongolian gerbil, Meriones
 RT unguliculatus: isolation, partial characterization, sequencing of cDNA,
 RT and implications for molecular evolution.";
 RL J. Biochem. 116:582-588 (1994).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; S77822; AAB33367.1; -;
 DR PIR; JX0346; JX0346.
 DR HSSP; P01009; IQLP.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR00215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
 KW SEQUENCE 406 AA; 45126 MW; 814613E44C7AA469 CRC64;
 SQ
 Query Match 19.6%; Score 417; DB 11; Length 406;
 Best Local Similarity 30.0%; Pred. No. 4.1e-24;
 Matches 114; Conservative 83; Mismatches 151; Indels 32; Gaps 11;
 QY 54 LAAVSNFGDYVRSMSPTNVLSPSLSVATLSALSLGAEQRTESIIRALYYDL- 112
 DB 39 MASNLDAFAGLYVLSHQSNNTNIFLSPLSIATAMLSLGSKDDTKAQLQGLHFNLT 98
 QY 113 -ISSPDHGYKELLDVTAPQKVL--SASRVFEKKLRKISFVAPLEKSYGTRPRVL 169
 DB 99 ETSEADIKGFQHLKLTNRPNDELQLTGSSLFVNNLSNLVEKFLVEEVKNHYHSEAFV 158
 QY 170 TGNRLDLQE----INNVAQAKMGKLARSTKIPDEISILLGVAFHFGQWTKDTSRK 225
 DB 159 N---FASBEAKTINFEVKAHGKIVDLVVKLEIDTVALVNYIFFRGKWEKPDPEL 215
 QY 226 TSLEDFYLDERTVVRVPMSPDKAVLYGL-----DSLSCKIAQLPTGSMIIIFLPL 280
 DB 216 TEEADFHVDKSTTVKVPWN-----RMGMFVHYCDTLSSWVLLMDYLGNAFAIFLPD 269
 QY 281 KVTQNLTLIEBSLTSETHIDRELKTVQAVLTVPKLKSVEGEVTKSLQEMKLSLF-D 339
 DB 270 E--GKQHLQTLTKHEHYKFLQNRHTRSANVHLPLSLISGTYNLKKVSLGITQVFN 327
 QY 340 SPDFSKI-TGKPIKLTQVEHRAGFEMNEDG---AGTTPSPGLQPAHLTPPLDYHLNQPTI 395
 DB 328 GADLSGITDVPKLSKXVHKAVLTLDERTGAAGTIV--LEAVPMSIPDPVCFKXNPFV 384
 QY 396 FVLRTDTGALLFIKILDP 415
 DB 385 VIICKHKTQSPFLVGVKNP 404

RESULT 15

Q91WP6

ID Q91WP6

AC Q91WP6;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Serine protease inhibitor 2-2.

GN SERPINA3N

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (SSP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; BC013651; AAH13651.1; -;
 DR HSSP; P01009; IQLP.
 DR MGI; MGI:105045; Serpina3n.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR00215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
 KW SEQUENCE 418 AA; 46718 MW; 4BF21BBEL0A91F6C CRC64;
 SQ
 Query Match 19.5%; Score 416.5; DB 11; Length 418;
 Best Local Similarity 28.7%; Pred. No. 4.7e-24;
 Matches 115; Conservative 85; Mismatches 180; Indels 21; Gaps 10;
 QY 33 PDST----GALVEEDPFFKVPVKNKLAASVNFQDYLYRVSSMSPTNVLSPSLVATA 88
 DB 22 PDGTLGMDAAVQEDHDNGTQDLSLTLASINTDFASLYKELVLPKPNKIVFSPLSISAA 81
 QY 89 LSALSGLGAEQRTESIIRALYYDL--ISSPDHGYKELLDVTAP--QXNLKASRIVF 144
 DB 82 LAVMSLGAAGNTLSEILEGLKFNLTETSEADIHQGFCHLLQRLNQPKDQVISTGSALFI 141
 QY 145 EKXURIKSFVAPLEKSYGTRPRVLTN---PRLDQEIINNVAQAKMGKLARSTKEIPD 201
 DB 142 EKQQLITFEQEKATLY--QAEAFADFOQROAKKLINDYVRKOTQGMKELVSLDK 199
 QY 202 EISILLGVAFHFGQWTKFDSRXTSLEDYLDERTVVRVPMSPDKAVLYRYGLSDLSLSC 261
 DB 200 RTLVLVNYIYFKAKWKVPFDPDLPDTFKSEFVAGKRRPVIVPMMSMEDLTTPYFRDELSLSC 259
 QY 262 KIAQLPTGSMIIIFLPLKVTQNLTLIEBSLTSETHIDRELK-TVQAVLTVPKLKS 320
 DB 260 TWELKYTGNASALFILPDQ--GSMQVQVSEASLOPETLRKWNKSLKPRMIDELHLPKFSIS 317
 QY 321 YEGEVTKSLQEMKLSLQSLFDS-PDFSKITG-KPIKLTQVEHRAGFEMNEDGAGITTPSPGLQ 378
 DB 318 TDYSLEDVLSKLGIREVFSTQADLSAITGKDLRSQVQVHKAVLDVAETGTEAAAAATGVK 377
 QY 379 PAHLT---FPLDYHLNQPFIFVLRTDTGALLFIKILDP 416
 DB 378 FVPMKAKLYPLTVYFNRPFLIMIFDTEIAPPIAKIANPK 418

Search completed: September 1, 2004, 11:17:33
 Job time : 124 secs